

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22910052_f3_310	3793	9015	145	438	290	3.2e-24

Protein name Locus Name Acc#
 sp:HELA_LEGPN Q48815

Description

HELA PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22915938_c1_408	3794	9016	240	723	86	0.0040

Protein name Locus Name Acc#
 hypothetical protein APE0978 pir:B72695 B72695

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23470135_f3_270.....	3795	9017	779	2340	695	7.6e-108

Protein name Locus Name Acc#
 sp:HEXA_PORGI P49008

Description

(BETA-NAHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23538425_f3_285.....	3796	9018	580	1743	561	1.4e-62

Protein name Locus Name Acc#
 long-chain-fatty-acid CoA ligase pir:D70386 D70386

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23601701_f3_289	3797	9019	69	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23625912_f3_280	3798	9020	477	1434	127	2.8e-07

Protein name

Locus Name

Acc#

gp:YP102KB

AL031866

Description

Yersinia pestis 102 kbases unstable region: from 1 to 119443.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23627187_c1_420	3799	9021	423	1272	158	1.0e-08

Protein name

Locus Name

Acc#

sp:FECR_ECOLI

P23485

Description

FECR PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23945430_c3_604	3800	9022	743	2232	228	1.0e-27

Protein name

Locus Name

Acc#

conserved hypothetical protein ylbK

pir:H69874

H69874

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24072712_c3_613	3801	9023	196	591	138	2.1e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein s110687	pir:S74416	S74416

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
243.9156.2_F3_2.72	3802	9024	437	1314	327	2.0e-29

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
N-acetyl muramoyl-L-alanine amidase	pir:G70445	G70445

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
243.98402_c3_56.4	3803	9025	98	297	225	1.3e-18

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:RS18_BACST	P10806

Description

30S RIBOSOMAL PROTEIN S18 (BS21)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24407802_c3_61.7	3804	9026	447	1344	164	1.0e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:NANH_MICVI	Q02834

Description

SIALIDASE PRECURSOR, (NEURAMINIDASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24615811_f1_10	3805	9027	458	1377	1028	1.0e-103

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ArgE/DapE/Acyl family protein	pir:E75324	E75324

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24645311_f1_52	3806	9028	299	900	147	6.9e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein aq_1533	pir:A70433	A70433

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648437_f1_103	3807	9029	297	894	211	1.0e-15

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
acriflavin resistance protein AcrE	pir:A70361	A70361

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24650287_c3_534	3808	9030	400	1203		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24660412_f3_325	3809	9031	350	1053	609	2.6e-59

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein TM1269	pir:D72274	D72274

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24706575_c2_496	3810	9032	63	192		
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<u>Protein name</u>	<u>Locus Name</u>
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<u>Acc#</u>

<u>Description</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24707287_c1_3.76.....	3811	9033	349	1050	894	1.6e-89
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<u>Protein name</u>	<u>Locus Name</u>
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<u>Acc#</u>

gp:PGU60208	U60208
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<u>Description</u>

Porphyromonas gingivalis orf1, orf2 and orf3 genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24804187_f2_179.....	3812	9034	76	231	91	0.0011
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<u>Protein name</u>	<u>Locus Name</u>
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<u>Acc#</u>

sodium channel protein	gp:DVU26718
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U26718

<u>Description</u>

Drosophila virilis sodium channel protein (para) gene, exons1,2,3,4, and optional segment i, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24806501_f2_190.....	3813	9035	146	441	71	0.038
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<u>Protein name</u>	<u>Locus Name</u>
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<u>Acc#</u>

hypothetical protein BBA32	pir:H70210
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H70210

<u>Description</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2533590_f2_196	3814	9036	82	249	68	0.034

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
cellulose synthase	pir:139714	I39714

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25431562_c1_3.7.1	3815	9037	237	714	1212	3.2e-123

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
rprY protein	pir:S33662	S33662

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25520626_c1_3.7.5	3816	9038	449	1350	776	5.2e-77

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YQEV_BACSU	P54462

<u>Description</u>						
HYPOTHETICAL 51.7 KD PROTEIN IN DNAJ-RPSU INTERREGIONIC REGION						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25674157_c1_3.7.8	3817	9039	81	246		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25975012_c1_3.9.3	3818	9040	311	936	158	4.8e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sodium-dependent transporter homolog yocS	pir:E69902	E69902

<u>Description</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2626655_C2_462	3819	9041	159	480		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26.3.0.6.5.0.7...c3...6.0.7.....	3820	9042	633	1902	1817	2.5e-187

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp: MUTB_PORGI	Q59676
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Description

METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT, (MCM-ALPHA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26.3.6.6.5.5...f3...3.26.....	3821	9043	476	1431	1177	1.7e-119

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein TM1267	pir:B72274	B72274
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26.3.7.0.3.0.2...f2...152.....	3822	9044	449	1350	1232	2.5e-125

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp: G6PA_BACST	P13375
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Description

ISOMERASE A)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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26642932_c2_450	3823	9045	60	183		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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28646.93_f3_306.....	3824	9046	442	1329	340	3.5e-62
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Protein name

Locus Name

Acc#

sp:QUEA_ECOLI

P21516

Description

(QUEUOSINE BIOSYNTHESIS PROTEIN QUEA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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29423.9.10_c2_522.....	3825	9047	81	246		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3.126.0.93.8_f3_261.....	3826	9048	591	1776	1242	2.1e-126
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Protein name

Locus Name

Acc#

sp:SYK_BACSU

P37477

Description

LYSYL-TRNA SYNTHETASE, (LYSINE--TRNA LIGASE) (LYSRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31289536_f2_164	3827	9049	110	333	83	0.0014

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
cytochrome oxidase I	gp:AF072662	AF072662

Description

Exoneurella eremophila cytochrome oxidase I gene, mitochondrial gene encoding mitochondrial protein, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31428541_f3_292	3828	9050	183	552	126	5.7e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YHA2_EIKCO	P35649

Description

HYPOTHETICAL 66.3 KD PROTEIN IN HAG2 5'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31755000_f1_29.....	3829	9051	567	1704	1079	4.0e-109

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YIDE_HAEIN	P44472

Description

HYPOTHETICAL PROTEIN HI0035

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31808567_c3_568.....	3830	9052	311	936	160	3.1e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable lipid A biosynthesis acyltransferase	pir:H71954	H71954

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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33397175_c2_529	3831	9053	633	1902		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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33.7.8.7.8.7.7_c1_35.8.....	3832	9054	354	1065	122	0.00032
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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MutS-like protein	gp:SATRXA	AJ223480
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<u>Description</u>

Staphylococcus aureus trxA and uvrC genes and partial mutS and dhsC genes.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3.3.8.5.8.9.0_c3_58.7.....	3833	9055	161	486	99	0.0018
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein C56G2.15	pir:T15873	T15873
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<u>Description</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3.4.1.6.5.9.1.2_f3_30.7.....	3834	9056	177	534	175	2.5e-13
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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probable isomerase	pir:B70986	B70986
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<u>Description</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3.4.4.0.6.3.0.3_f1_87.....	3835	9057	191	576		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34411051_f3_300	3836	9058	728	2187	134	5.3e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:PGU60208	U60208

Description

Porphyromonas gingivalis orf1, orf2 and orf3 genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34417142_c1_414	3837	9059	717	2154	3088	0.0

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp: MUTA_PORGI	Q59677

Description

METHYLMALONYL-COA MUTASE BETA-SUBUNIT, (MCB-BETA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.56.61441_f3_251.....	3838	9060	72	219		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.6.1.346.57_f1_90.....	3839	9061	201	606	300	1.4e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein PAB0910	pir:B75048	B75048
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
37562_c2_530	3840	9062	912	2736	506	5.4e-56

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
37785_c3_611.....	3841	9063	264	795	107	0.00081

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein SCE39.30	pir:T36240	T36240

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3944087_c2_451.....	3842	9064	392	1179	153	4.9e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein c0115	pir:S74051	S74051

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4068777_c2_463.....	3843	9065	578	1737	801	6.8e-84

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:EFG_THETH	P13551

Description

ELONGATION FACTOR G (EF-G)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4078910_c3_614	3844	9066	1175	3528	519	8.8e-60

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (RagA)	gp:PGI130872	AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
41562_c3_571	3845	9067	66	201		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
426657_c3_612.....	3846	9068	144	435	268	8.6e-22

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
proline/pyrroline-5-carboxylate dehydrogenase	pir:B71980	B71980

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4329428_f3_265.....	3847	9069	245	738	255	8.4e-22

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YFBT_ECOLI	P77625

Description

HYPOTHETICAL 23.7 KD PROTEIN IN LRHA-ACKA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4378530_f1_21	3848	9070	485	1458	468	2.2e-44

Protein name Locus Name Acc#

probable glycosyl hydrolase pir:T36467 T36467

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4532885_c3_593.....	3849	9071	171	516	96	0.0057

Protein name Locus Name Acc#

putative outer surface protein gp:BBU80960

Description

Borrelia burgdorferi strain CA12 putative outer membrane protein(ospE) gene, complete cds and putative outer surface protein (ospF) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4551635_f1_102.....	3850	9072	1285	3858	1850	1.7e-192

Protein name Locus Name Acc#

czrA protein gp:PACZR Y14018

Description

Pseudomonas aeruginosa czrR, czrC, czrB, czrA genes, ORF5 andpartial ORF6.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4698910_f3_275.....	3851	9073	892	2679	476	3.4e-78

Protein name Locus Name Acc#

ribonucleoside-diphosphate reductase, large chain nrn pir:G69457 G69457

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4704675_f2_169	3852	9074	905	2718	1036	2.5e-145

Protein name Locus Name Acc#
 4-alpha-glucanotransferase homolog T20B5.4 pir:T00748 T00748
Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
48.045.3.7_f1_65.....	3853	9075	149	450	197	1.2e-15

Protein name Locus Name Acc#
sp:FOLB_BACSU P28823
Description

DIHYDRONEOPTERIN ALDOLASE, (DHNA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
486.7.188_c1_415.....	3854	9076	719	2160	883	2.4e-88

Protein name Locus Name Acc#
sp:TOP3_HAEIN P43704
Description

DNA TOPOISOMERASE III,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
488.228.7_f2_188.....	3855	9077	385	1158	599	2.9e-58

Protein name Locus Name Acc#
 coproporphyrinogen oxidase, III,
 oxygen-independent hemN pir:B69640 B69640
Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4892261_c2_466	3856	9078	155	468	271	1.7e-23

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ribosomal protein L09	pir:B70475	B70475

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
48.9.7125..f3..262.....	3857	9079	334	1005	403	1.7e-37

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:GPDA_BACSU	P46919

Description

DEPENDENT DIHYDROXYACETONE-PHOSPHATE REDUCTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
49.75625..f1..91.....	3858	9080	128	387		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.11.7.76.3..c1..3.8.9.....	3859	9081	261	786	287	3.4e-25

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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probable reductase APE1044	pir:E72703	E72703
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Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5859380_f3_288	3860	9082	173	522	136	3.4e-09

Protein name	Locus Name	Acc#
unknown	gp:AF095748	AF095748

Description

Burkholderia cepacia principal sigma factor (sigA), phthalatedioxygenase reductase (ophA1), putative phthalate permeaseN-terminal region, putative phthalate permease C-terminal region(ophD), 4,5-dihydroxyphthalate decarboxylase (ophC), phthalate-inducible quinolinate phosphoribosyl transferase (ophE),transposase (tnp), phthalate dihydrodiol dehydrogenase

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5866512_c3_531.....	3861	9083	226	681		

Protein name	Locus Name	Acc#
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6.031717_c1_370.....	3862	9084	154	465	321	6.3e-28

Protein name	Locus Name	Acc#
translation elongation factor G	pir:H72227	H72227

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6.136675_c3_561.....	3863	9085	527	1584	2624	7.7e-273

Protein name	Locus Name	Acc#
RprX	gp:S59000	S59000

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
625087_f1_53	3864	9086	488	1467	700	8.9e-78

Protein name Locus Name Acc#
sp:DNAA_BACSU P05648

Description

CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6447131_f1_44	3865	9087	221	666	669	1.1e-65

Protein name Locus Name Acc#
sp:UNG_HUMAN P13051

Description

URACIL-DNA GLYCOSYLASE PRECURSOR, (UDG)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
645483.7_c2_477.....	3866	9088	176	531	352	4.4e-32

Protein name Locus Name Acc#
methylglyoxal synthase pir:G72284 G72284

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
68293.87_f2_189.....	3867	9089	189	570	176	2.0e-13

Protein name Locus Name Acc#
probable RNA polymerase sigma-24 factor (rpoE) pir:E71368 E71368

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6837762_c2_502	3868	9090	179	540	167	1.8e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:Y778_METJA	Q58188

Description

HYPOTHETICAL PROTEIN MJ0778

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
954787_f1_43	3869	9091	375	1128	828	1.6e-82

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ASNA_HAEIN	P44338

Description

ASPARTATE--AMMONIA LIGASE, (ASPARAGINE SYNTHETASE A)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9782217_f2_145.....	3870	9092	211	636	84	0.047

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:Y804_HAEIN	P44053

Description

HYPOTHETICAL PROTEIN HI0804

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11720063_c3_96.....	3871	9093	519	1560	695	2.0e-68

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
alpha galactosidase precursor	gp:AF061331	AF061331

Description

Saccharopolyspora erythraea alpha galactosidase precursor (melA) gene, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12688787_f3_50	3872	9094	167	504	215	1.4e-17

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
cytidine deaminase	gp:BCA237979	AJ237979

Description

Bacillus caldolyticus cdd gene for cytidine deaminase.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12773337_c1_77	3873	9095	426	1281	142	1.1e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein yknZ	pir:E69858	E69858

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13845217_f3_57.....	3874	9096	81	246		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14569175_f3_55.....	3875	9097	329	990	401	2.8e-37

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF083252	AF083252

Description

Pseudomonas aeruginosa enoyl-CoA hydratase gene, partial cds; pilin biosynthetic protein (fimL) gene, complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21665630_f2_34	3876	9098	213	642	448	3.0e-42

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YKGB_HAEIN	P44577

Description

HYPOTHETICAL PROTEIN HI0219

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22144041_f2_33	3877	9099	287	864	233	1.8e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
PobR protein	gp:PPU251792	AJ251792

Description

Pseudomonas putida pobR gene for PobR protein and pobA gene for PobA protein.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
223.05443...c3...94.....	3878	9100	478	1437	123	0.00026

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:U96771	U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
237.9442_f1_13.....	3879	9101	467	1404	970	1.4e-97

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YKGC_ECOLI	P77212

Description

INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24095327_c3_106	3880	9102	299	900	627	3.2e-61

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hemagglutinin	gp:AF017417	AF017417

Description

Prevotella intermedia hemagglutinin (phg) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24642687_c1_66	3881	9103	300	903	547	9.5e-53

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:DCHS_CLOPE	P04194

Description

HISTIDINE DECARBOXYLASE PROENZYME PRECURSOR, (PI CHAIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24.719.017_c3_95.....	3882	9104	156	471		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25.8.7.9.0.8_c3_109.....	3883	9105	430	1293	182	4.2e-11

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
YvrN protein	gp:BS43KBDNA	AJ223978

Description

Bacillus subtilis 42.7KB DNA fragment from yvsA to yvqA.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26595051_c3_108	3884	9106	417	1254	184	1.7e-11

Protein name Locus Name Acc#

hypothetical protein aq_294 pir:H70326 H70326

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.05.0415.7..±2..35.....	3885	9107	531	1596	779	2.5e-77

Protein name Locus Name Acc#

putative ABC transporter ATP-binding protein gp:SCF56 AL133424

Description

Streptomyces coelicolor cosmid F56.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.64.627.76..c1..64.....	3886	9108	112	339		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4.3.0.6.26.8..±3..6.1.....	3887	9109	63	192	72	0.020

Protein name Locus Name Acc#

ORF MSV147 hypothetical protein gp:AF063866 AF063866

Description

Melanoplus sanguinipes entomopoxvirus, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
676677_c3_93	3888	9110	194	585	159	3.0e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (RagA)	gp:PGI130872	AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
975050_c1_78	3889	9111	160	480		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1197324_c1_98.....	3890	9112	155	468	267	8.0e-23

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
endo-beta-galactosidase	gp:AF083896	AF083896

Description

Flavobacterium keratolyticus endo-beta-galactosidase gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11975307_c3_184.....	3891	9113	71	216	230	3.7e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
rubredoxin	pir:H72348	H72348

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14354208_c3_195	3892	9114	423	1272		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15.7.126.83...E2...6.9.....	3893	9115	66	201		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16.6.1.713.5...C3...1.7.7.....	3894	9116	70	213		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16.9.14.0.7.7...E3...9.4.....	3895	9117	262	789	147	4.3e-10

Protein name Locus Name Acc#

ORF8 gp:D78257 D78257

Description

Enterococcus faecalis plasmid pYI17 genes for BacA, BacB, ORF3, ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21660966_c2_163	3896	9118	140	423	112	2.4e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF116463	AF116463

Description

Streptomyces lincolnensis putative regulatory protein WdIA (wdIA) gene, complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21756552_f2_67	3897	9119	217	654		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
222.7.0327_c2_130.....	3898	9120	304	915	332	5.8e-30

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein slr1534	pir:S75855	S75855

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
223.6.09.00_c1_124.....	3899	9121	64	195		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23446055_c1_116	3900	9122	610	1833		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
236.9.7.132...f2...49.....	3901	9123	646	1941		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
242.7.53.8.0...c2...16.7.....	3902	9124	188	567	483	5.8e-46

Protein name Locus Name Acc#

phosphoribosylaminoimidazole carboxylase
(pure) PAB1077

pir:B75013 B75013

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
244.0.7.53.0...f1...8.....	3903	9125	157	474		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24409383_f1_31	3904	9126	214	645	234	1.4e-19

Protein name Locus Name Acc#

hypothetical 23.5K protein (glnA-fdhE intergenic region):hypothetical protein o206	pir:S40829
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2461693_f1_18	3905	9127	612	1839	127	1.6e-13

Protein name Locus Name Acc#

hypothetical protein SC6C5.12c SC6C5.12c	pir:T35483	T35483
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648516_c1_114	3906	9128	559	1680	1192	4.3e-121

Protein name Locus Name Acc#

uridine kinase-related protein	pir:B72341	B72341
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24666412_f2_64	3907	9129	333	1002	527	1.3e-50

Protein name Locus Name Acc#

riboflavin kinase	pir:D70313	D70313
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25682030_f1_1	3908	9130	185	558	310	1.2e-27

Protein name Locus Name Acc#

hypothetical protein	pir:F72424	F72424
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29861251_c1_115	3909	9131	526	1581	224	1.1e-15

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sensor histidine kinase	pir:A72383	A72383

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.01265.00_f2_6.3	3910	9132	562	1689	664	2.4e-64

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ATC1_DICDI	P54678

Description

CATION-TRANSPORTING ATPASE PAT1,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.05.096.32_f1_2.8	3911	9133	575	1728	568	3.1e-54

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sensory transduction histidine kinase slr2104:protein slr2104:protein slr2104	pir:S75136	S75136

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.16.74158_f1_1.7	3912	9134	90	273		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31835967_f2_47	3913	9135	515	1548	411	1.1e-50

<u>protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
aminopeptidase	gp:AF041033	AF041033

Description

Shigella flexneri aminopeptidase (pepP) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32219042_c3_196	3914	9136	496	1491	496	2.4e-47

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:RP54_ACICA	P33983

Description

RNA POLYMERASE SIGMA-54 FACTOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.3.9.0.93.7_f3_95.....	3915	9137	80	243	267	4.5e-23

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transcription regulator homolog yozG	pir:C69931	C69931

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.3.9.92212_c3_199.....	3916	9138	490	1473	665	3.0e-65

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
gcpe protein	pir:E72087	E72087

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34486592_f2_51	3917	9139	224	675		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35441251_c1_99.....	3918	9140	389	1170	190	2.6e-12

Protein name Locus Name Acc#

sp:QPCT_HUMAN

Description

(GLUTAMINYL-TRNA CYCLOTRANSFERASE) (GLUTAMINYL CYCLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36413327_f1_30.....	3919	9141	348	1047	538	2.7e-64

Protein name Locus Name Acc#

calcium motive P-type ATPase gp:AF145282 AF145282

Description

Trichomonas vaginalis calcium motive P-type ATPase (CA-2) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4328175_c1_100.....	3920	9142	145	438	251	2.2e-21

Protein name Locus Name Acc#

sp:YE19_SYNY3 P74523

Description

HYPOTHETICAL 17.7 KD PROTEIN SLR1419

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4334562_c3_198	3921	9143	130	393	339	1.0e-30

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:GCSH_ECOLI	P23884

Description

GLYCINE CLEAVAGE SYSTEM H PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4475705_f1_14	3922	9144	180	543		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4724062_c3_197.....	3923	9145	235	708	157	2.0e-11

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:Y61A_METJA P81310

Description

HYPOTHETICAL PROTEIN MJ0611.1

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
81887_c1_128.....	3924	9146	230	693	356	4.6e-36

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein gcpE pir:E71562 E71562

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9782828_f2_52	3925	9147	145	438		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9.92.9832_E3_8.9.....	3926	9148	565	1698	739	4.3e-73

Protein name Locus Name Acc#

conserved hypothetical integral membrane protein TP0771

pir:H71283 H71283

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10003452_c3_6.3.2.....	3927	9149	551	1656	338	1.2e-27

Protein name Locus Name Acc#

sp:YICI_ECOLI

Description

HYPOTHETICAL 88.1 KD PROTEIN IN GLTS-SELC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
100400_c2_481.....	3928	9150	108	327		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10188427_f3_266	3929	9151	72	219	103	8.7e-05

Protein name Locus Name Acc#
 transposase gp:AF038866 AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) andmobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10291393_f1_12	3930	9152	464	1395	800	1.5e-79

Protein name Locus Name Acc#
 sp:Y260_SYNY3 P74409

Description

HYPOTHETICAL 49.2 KD PROTEIN SLL0260

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10.7193.85....f3....3.18.....	3931	9153	97	294		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10.73.93.87....f3....3.3.0.....	3932	9154	469	1410	263	2.1e-20

Protein name Locus Name Acc#
 transposase gp:AF038866 AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) andmobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10739526_c1_416	3933	9155	713	2142	837	2.9e-110

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
alpha-glucosidase	gp:BTU66897	U66897

Description

Bacteroides thetaiotaomicron neopullulanase (susA) and alpha-glucosidase (susB) genes, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10979675_f1_20	3934	9156	620	1863	174	2.4e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable purine NTPase PAB0812	pir:F75103	F75103

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11016386_f1_116.....	3935	9157	74	225		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
112686_f1_13.....	3936	9158	169	510		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1209436_f2_211	3937	9159	391	1176	493	5.0e-47

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive 42kD antigen PG33	gp:AF175715	AF175715

Description

Porphyromonas gingivalis strain W50 immunoreactive 42kD antigenPG33 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12316382_c2_553	3938	9160	167	504	477	2.5e-45

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
O-acetylhomoserine sulfhydrylase	pir:D72324	D72324

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12516.930_f3_291	3939	9161	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12582.785_f3_281	3940	9162	68	207		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12690927_c3_555	3941	9163	332	999	299	4.2e-36

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein F19D11.16:hypothetical protein F14M4.29:hypothetical protein F14M4.29	pir:T02689	

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12897701_c3_642.....	3942	9164	257	774	748	4.8e-74

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
O-acetylhomoserine sulfhydrylase	pir:D72324	D72324

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13835817_f3_315.....	3943	9165	64	195		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14063318_f2_207.....	3944	9166	60	183	129	1.9e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PH1147	pir:E71056	E71056

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14156287_f3_255	3945	9167	445	1338	168	4.4e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:PGU60208	U60208

Description

Porphyromonas gingivalis orf1, orf2 and orf3 genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14463437_c3_592	3946	9168	234	705	200	5.6e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein ycgF	pir:A69758	A69758

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14745312_f3_290.....	3947	9169	103	312	77	0.013

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
NADH dehydrogenase subunit 2	gp:AF160864	AF160864

Description

Tetrahymena pyriformis mitochondrial DNA, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15079802_f1_100.....	3948	9170	106	321		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

<u>NO-HIT</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15631502_f1_99	3949	9171	442	1329	300	1.2e-33

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YHCG_ECOLI	P45423

Description

HYPOTHETICAL 43.3 KD PROTEIN IN GLTF-NANT INTERGENIC REGION (O375)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15707788_c2_535	3950	9172	268	807	386	1.1e-35

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transposase	gp:AF038866	AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) andmobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16229142_c2_509	3951	9173	75	228		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16493968_c1_455	3952	9174	331	996	204	3.4e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:XYNC_CALSA	P23553

Description

ACETYL ESTERASE, (ACETYLXYLOSIDASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16594202_f1_73	3953	9175	62	189		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16.8.32885_f3_339	3954	9176	431	1296	1723	2.3e-177

Protein name _____ Locus Name _____ Acc# _____

hypothetical protein _____ pir:JQ1020 JQ1020

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
18.7.826_f3_271	3955	9177	746	2241	2313	6.9e-240

Protein name _____ Locus Name _____ Acc# _____

sp:PFL_CLOPA Q46266

Description

FORMATE ACETYLTRANSFERASE, (PYRUVATE FORMATE-LYASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19.54562_c3_6.05	3956	9178	1111	3336	557	5.9e-55

Protein name _____ Locus Name _____ Acc# _____

115K outer membrane protein precursor:SusC protein pir:JC6027 JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19617202_c3_559	3957	9179	68	207		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
197.06258_c2_541	3958	9180	76	231	143	4.0e-09

Protein name Locus Name Acc#

transposase gp:AF038866 AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) andmobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
198.7817_c1_388	3959	9181	79	240		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20039010_c2_537	3960	9182	130	393		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20213303_c2_519	3961	9183	394	1185	161	7.1e-16

Protein name Locus Name Acc#
 ATP-dependent activating enzyme gp:PFFBSCEAB Y09356

Description
 Pseudomonas fluorescens fbsC, fbsE, fbsA and fbsB genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2031290_f1_25	3962	9184	70	213		

Protein name Locus Name Acc#
Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20319132_c2_523.....	3963	9185	354	1065	159	3.0e-10

Protein name Locus Name Acc#
 transmembrane sensor gp:AF051691 AF051691

Description
 Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20353400_f1_107.....	3964	9186	833	2502	801	1.2e-79

Protein name Locus Name Acc#
Description sp:MUS2_BACSU P94545

MUTS2 PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20801930_c2_505	3965	9187	512	1539	467	3.9e-51

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
amidophosphoribosyltransferase	pir:H69185	H69185

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2125277_f1_113	3966	9188	526	1581	2616	5.4e-272

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
alkyl hydroperoxide reductase subunit F	gp:AF129406	AF129406

Description

Bacteroides fragilis alkyl hydroperoxide reductase subunit C (ahpC) and alkyl hydroperoxide reductase subunit F (ahpF) genes, completecds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2146927_f1_11	3967	9189	282	849	410	3.1e-38

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transcription regulator yggG	pir:G65078	

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21605288_f2_134	3968	9190	874	2625	93	0.0019

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein b2228	pir:B64993	B64993

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21722925_c2_496	3969	9191	95	288		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
218.78.05_c2_507	3970	9192	64	195	75	0.019

Protein name Locus Name Acc#

putative transmembrane protein gp:SCU96107 U96107

Description

Staphylococcus carnosus N5,N10-methylenetetrahydromethanopterin reductase homolog, SceB precursor (sceB) and putative transmembrane protein genes, complete cds, and putative Na⁺/H⁺ antiporter NhaC(nhaC) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
220.44.07_f1_103	3971	9193	322	969	87	0.045

Protein name Locus Name Acc#

sp:PRIM_LISMO P47762

Description

DNA PRIMASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22289.06.1_f2_142	3972	9194	106	321		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22539088_c3_593	3973	9195	186	561		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22689628_f2_204	3974	9196	72	219		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f1_106	3975	9197	83	252	64	0.031

Protein name Locus Name Acc#

sp:SPRC_XENLA P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22928812_c1_441	3976	9198	65	198		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23445317_c1_458	3977	9199	310	933	721	3.5e-71

Protein name Locus Name Acc#
 conserved hypothetical protein BB0682 pir:A70185 A70185

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
236.095.1.7_c3_613.....	3978	9200	358	1077	508	1.3e-48

Protein name Locus Name Acc#
 gp:A00047 A00047

Description

E.coli mor gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
236.347.01_c1_424.....	3979	9201	308	927	113	3.4e-06

Protein name Locus Name Acc#
 AmpG-signal transducer gp:ECAMPG3 X82159

Description

E.coli ampG3 gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
236.406.7.5_c1_364.....	3980	9202	165	498	101	0.0025

Protein name Locus Name Acc#
 hypothetical protein A208R pir:T17698 T17698

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2378150_c3_595	3981	9203	532	1599	1332	6.2e-136

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:RF3_ECOLI	P33998

Description

PEPTIDE CHAIN RELEASE FACTOR 3 (RF-3)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23945263_f3_275	3982	9204	257	774		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24093763_c1_398.....	3983	9205	417	1254	1298	2.5e-132

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:PEPT_BACSU	P55179

Description

PEPTIDASE T, (AMINOTRIPEPTIDASE) (TRIPEPTIDASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24229677_c1_375.....	3984	9206	339	1020	1381	4.0e-141

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
class A beta-lactamase CFXA2 precursor	gp:AF118110	AF118110

Description

Prevotella intermedia class A beta-lactamase CFXA2 precursor (cfxA2) gene, complete cds.
--

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24397187_c3_562	3985	9207	186	561		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24414.026_t2_15.0	3986	9208	164	495	390	4.1e-36

Protein name Locus Name Acc#

Dps gp:AB025779 AB025779

Description

Porphyromonas gingivalis gene for Dps, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24429.050_c1_40.3	3987	9209	769	2310	465	1.9e-43

Protein name Locus Name Acc#

sp:YBAL_ECOLI

Description

HYPOTHETICAL 59.4 KD PROTEIN IN GSK-FSR INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
246446.37_c2_46.0	3988	9210	301	906	168	7.1e-10

Protein name Locus Name Acc#

nucleotide pyrophosphatase homolog T16L4.210 pir:T09933 T09933

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24782792_c3_608	3989	9211	395	1188		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24804817_c3_6.0.7	3990	9212	246	741	123	3.2e-05

Protein name Locus Name Acc#

sp:EBA2_FLAME P36912

Description

(ENDOGLYCOSIDASE F2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24807812_f1_108	3991	9213	357	1074	528	9.8e-51

Protein name Locus Name Acc#

divalent cation transport-related protein pir:H72360 H72360

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24822142_f2_226	3992	9214	190	573		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24848928_c1_459	3993	9215	66	201		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24849132_f3_335	3994	9216	374	1125		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25.00.052_c2_513	3995	9217	423	1272	376	1.3e-34

Protein name Locus Name Acc#

sp:YIDA_ECOLI

Description

HYPOTHETICAL 29.7 KD PROTEIN IN IBPA-GYRB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
253.98.385_c2_461	3996	9218	346	1041	262	1.5e-22

Protein name Locus Name Acc#

hypothetical protein F14F9.5 pir:T33774 T33774

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25422162_f1_5	3997	9219	278	837		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
255.8.0212_f1_97	3998	9220	76	231	78	0.034

Protein name Locus Name Acc#

HCG-1 protein gp:AF044219 AF044219

Description

Drosophila melanogaster HCG-1 protein (HCG-1) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
258.92062_c2_498	3999	9221	111	336	173	4.1e-13

Protein name Locus Name Acc#

thioredoxin-like protein gp:ATAC010718 AC010718

Description

Arabidopsis thaliana chromosome I BAC F28O16 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
258.92187_c3_594	4000	9222	291	876	593	1.3e-57

Protein name Locus Name Acc#

probable dTDP-L-rhamnose synthase pir:T31087 T31087

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26359635_c1_409	4001	9223	373	1122	280	1.9e-24

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ENTC_ECOLI	P10377

Description

ISOCHORISMATE SYNTHASE ENTC,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26460003_c3_599	4002	9224	579	1740	454	6.8e-43

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:MEND_HAEIN	P44612

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26461680_c3_580.....	4003	9225	351	1056	614	7.6e-60

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable zinc-containing dehydrogenase	pir:T36961	T36961

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
266.0.03.27_c1_3.93.....	4004	9226	145	438	111	1.5e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ferric uptake regulation protein	pir:G72213	G72213

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26601677_c1_412	4005	9227	276	831	1012	5.1e-102

Protein name Locus Name Acc#
 naphthoate synthase, menB:DHNA
 synthase:dihydroxynaphthoate
 synthase:dihydroxynaphthoic acid synthetase

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26604687_f2_133	4006	9228	134	405		

Protein name Locus Name Acc#
Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26604692_c3_621	4007	9229	161	486	239	1.1e-19

Protein name Locus Name Acc#
 transposase gp:AF038866 AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) andmobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26820341_c3_603	4008	9230	331	996	140	9.2e-07

Protein name Locus Name Acc#
 Hyp1 protein gp:HVHYP1PRO Y09797

Description

H.vulgaris mRNA for Hyp1 protein.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29398290_f3_257	4009	9231	64	195	83	0.0053

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
asparagine-rich protein (clone 28C6)	pir:S14470	S14470

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.007.96.75_c3_583.....	4010	9232	805	2418	366	1.5e-31

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
Sensor protein RcsC (EC 2.7.3.-)	gp:D90850	

Description

E.coli genomic DNA, Kohara clone #373 (49.5-49.9 min.).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.0195142_c2_536.....	4011	9233	924	2775	323	8.8e-25

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:C72285	C72285

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.0502255_f2_127.....	4012	9234	344	1035		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
NO-HIT		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.0572331_c1_430.....	4013	9235	115	348		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
NO-HIT		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32478803_c2_552	4014	9236	110	333	80	0.033

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:CPE1_BOVIN	018963

Description

CYTOCHROME P450 2E1, (CYP11E1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32523576_f1_82	4015	9237	61	186		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.3.19.4.37...c3...6.28.....	4016	9238	173	522		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.3.21.09.36...f1...46.....	4017	9239	214	645	163	4.7e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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RNA polymerase sigma factor SigZ-like protein gp:AF137263 AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33400263_c1_423	4018	9240	338	1017		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33.7.86.0.83...E3...3.3.8.....	4019	9241	483	1452	2084	1.3e-215

Protein name Locus Name Acc#

NBU1 mobilization protein mob pir:A49901 A49901

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34.026.55B...t1_36.....	4020	9242	65	198		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
345.0.9.7.0.0_c1_422.....	4021	9243	137	414		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35.1.5.7.0.5.0...t2_227.....	4022	9244	327	984	236	8.6e-20

Protein name Locus Name Acc#

hypothetical protein PAB0040 pir:B75194 B75194

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
35161302_c2_524	4023	9245	211	636	158	1.0e-10

Protein name	Locus Name	Acc#
	sp:Y350_HAEIN	P24326

Description

HYPOTHETICAL PROTEIN HI0350 (ORF3)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36073591_c1_389	4024	9246	301	906	362	3.8e-33

Protein name	Locus Name	Acc#
	sp:YZ09_MYCTU	Q10543

Description

HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE CY31.09,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3.6.20.7.933_c1_413.....	4025	9247	355	1068	175	1.1e-10

Protein name	Locus Name	Acc#
chloromuconate cycloisomerase homolog ykfB	pir:H69855	H69855

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3.6.36.10.02_f3_26.7.....	4026	9248	169	510		

Protein name	Locus Name	Acc#
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3944688_f3_349	4027	9249	191	576	983	6.0e-99

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
alkyl hydroperoxide reductase subunit C	gp:AF129406	AF129406

Description

Bacteroides fragilis alkyl hydroperoxide reductase subunit C (ahpC) and alkyl hydroperoxide reductase subunit F (ahpF) genes, completecds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3947562_c2_534	4028	9250	400	1203	758	4.2e-75

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transposase	gp:AF038866	AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) andmobilization protein BmpH (bmpH) genes, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4094563_f2_137.....	4029	9251	445	1338	128	5.1e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PH0922	pir:D71082	D71082

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4094687_c1_411.....	4030	9252	337	1014		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4094800_f3_344	4031	9253	405	1218	698	4.8e-83

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:SDHL_STRCO	086564

Description

L-SERINE DEHYDRATASE, (L-SERINE DEAMINASE) (SDH) (L-SD)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4504682_c1_402	4032	9254	250	753	131	1.4e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
intracellular hyaluronic acid binding protein	gp:AF032862	AF032862

Description

Homo sapiens intracellular hyaluronic acid binding protein (IHABP)mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4.719626...c2...508.....	4033	9255	592	1779		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4800926_f3_326.....	4034	9256	512	1539	356	5.6e-31

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:GA6S_HUMAN	P34059

Description

(CHONDROITINASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4939000_c2_525	4035	9257	336	1011	1037	1.1e-104

Protein name Locus Name Acc#

conserved hypothetical protein pir:B72278 B72278

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.081927_c2_504.....	4036	9258	679	2040	1451	1.5e-148

Protein name Locus Name Acc#

cation-transporting atpase, p-type (pacs) pir:E75141 E75141
PAB0626

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.10.937_c1_36.5.....	4037	9259	171	516		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.11.77.62_c3_6.16.....	4038	9260	422	1269	114	0.000075

Protein name Locus Name Acc#

hypothetical protein F42G9.3 pir:T16348 T16348

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.16.7037_c3_6.06.....	4039	9261	518	1557		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5273552_c3_639	4040	9262	148	447		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5363816_c1_386	4041	9263	380	1143	104	0.0047

Protein name Locus Name Acc#

gp:PFMAL3P7

Description

Plasmodium falciparum MAL3P7, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
584700_f3_263	4042	9264	90	273		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6429643_c3_615	4043	9265	189	570	190	6.5e-15

Protein name Locus Name Acc#

sp:RPOE_HAEIN

P44790

Description

RNA POLYMERASE SIGMA-E FACTOR (SIGMA-24)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6444077_f1_27	4044	9266	241	726	555	1.4e-53

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:PFLA_ECOLI	P09374

Description

ACTIVATING ENZYME)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7084675_f1_19	4045	9267	387	1164		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7.109407_c3_586.....	4046	9268	135	408	253	1.4e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:YEAO_ECOLI P76243

Description

HYPOTHETICAL 14.2 KD PROTEIN IN GAPA-RND INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
8.6.092.7_c2_503.....	4047	9269	348	1047	668	1.4e-65

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:YEIH_ECOLI P33019

Description

HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
975780_f3_333	4048	9270	351	1056	93	0.0034

Protein name Locus Name Acc#

troponin T, cardiac muscle:troponin T2 pir:TPHUTC

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9927330_c3_627	4049	9271	63	192		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9954757_c3_561	4050	9272	189	570		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9959400_c1_399	4051	9273	367	1104	815	3.8e-81

Protein name Locus Name Acc#

sp:GCST_BACSU P54378

Description

T PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22438202_f2_1	4052	9274	74	222		

Protein name _____ Locus Name _____

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10556942_f3_138	4053	9275	634	1905	411	5.6e-38

Protein name _____ Locus Name _____

Acc#

inner membrane protein homolog

pir:A70155

A70155

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11125291_f3_146	4054	9276	191	576	137	2.7e-09

Protein name _____ Locus Name _____

Acc#

transcriptional regulator

gp:BSUB0017

Description

Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12931502_f3_166	4055	9277	143	432	222	2.6e-18

Protein name _____ Locus Name _____

Acc#

heat shock protein, class I

pir:D72385

D72385

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13860625_c2_279	4056	9278	113	342	78	0.0048

Protein name Locus Name Acc#

conserved hypothetical protein yuld pir:F70014 F70014

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14564.061_c1_196.....	4057	9279	438	1317	1171	7.2e-119

Protein name Locus Name Acc#

coenzyme F390 synthetase II pir:B69115 B69115

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1464.8587_c3_286.....	4058	9280	1033	3102	556	1.2e-50

Protein name Locus Name Acc#

sensory transduction histidine kinase slr2098:protein slr2098:protein slr2098 pir:S75130 S75130

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1466.7192_c2_90.....	4059	9281	737	2214	623	4.4e-72

Protein name Locus Name Acc#

Tri r 4 allergen gp:AF082514 AF082514

Description

Trichophyton rubrum Tri r 4 allergen mRNA, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
188135_c2_259	4060	9282	556	1671	264	1.0e-35

Protein name	Locus Name	Acc#
	sp:YCLF_BACSU	P94408

Description

HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19709682_c1_235	4061	9283	207	621	549	5.9e-53

Protein name	Locus Name	Acc#
CDP-4-keto-6-deoxy-D-glucose-3-dehydrase	pir:E47070	E47070

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19742217_f1_44.....	4062	9284	189	570		

Protein name	Locus Name	Acc#
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Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19785941_c2_237.....	4063	9285	476	1431	597	2.6e-103

Protein name	Locus Name	Acc#
	sp:YBHF_ECOLI	P75776

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBHF

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1992182_f2_107	4064	9286	112	339		

Protein name _____ Locus Name _____ Acc# _____

Description _____

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
201953.02..f3..161.....	4065	9287	452	1359	83	0.016

Protein name _____ Locus Name _____ Acc# _____

sp:YK58_YEAST P36158

Description _____

HYPOTHETICAL 68.3 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20321015..c2..242.....	4066	9288	61	186		

Protein name _____ Locus Name _____ Acc# _____

Description _____

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20364090..c3..324.....	4067	9289	958	2877	331	1.2e-25

Protein name _____ Locus Name _____ Acc# _____

hypothetical protein C26D10.4 pir:T19486 T19486

Description _____

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20595050..c2..261.....	4068	9290	409	1230	385	1.4e-35

Protein name _____ Locus Name _____ Acc# _____

hypothetical protein SC5C7.08 SC5C7.08 pir:T35215 T35215

Description _____

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21522003_c3_318	4069	9291	142	429		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22438202_c1_233	4070	9292	172	519	180	7.4e-14

Protein name Locus Name Acc#

unknown gp:AF048749 AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2246276.0_c2_238	4071	9293	367	1104	470	1.4e-44

Protein name Locus Name Acc#

sp:YBHS_ECOLI P75775

Description

HYPOTHETICAL 42.1 KD PROTEIN IN MOAE-RHLE INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2293045.0_c2_236	4072	9294	179	540	146	1.4e-09

Protein name Locus Name Acc#

sp:YHII_ECOLI P37626

Description

(F355)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23459636_f3_160	4073	9295	117	354		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23516.000...c1_213.....	4074	9296	93	282		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23594.055...c1_190.....	4075	9297	116	351	90	0.00026

Protein name _____ Locus Name _____ Acc# _____

sp:Y13B_BPT4 P17308

Description

HYPOTHETICAL 11.5 KD PROTEIN IN GP31-CD INTERGENIC REGION (ORF B)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23642175_f1_11.....	4076	9298	424	1275		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23926877_c1_214	4077	9299	485	1458		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23986.057_f1_22	4078	9300	447	1344	363	6.7e-36

Protein name Locus Name Acc#

damage-inducible protein PAB0243 pir:A75151 A75151

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24225316_c1_197	4079	9301	150	453	284	7.1e-25

Protein name Locus Name Acc#

hypothetical protein MTH1854 pir:A69115 A69115

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24257.937_c1_204	4080	9302	363	1092	117	2.1e-06

Protein name Locus Name Acc#

hypothetical protein PAB0603 pir:E75137 E75137

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24400.285_f3_156	4081	9303	259	780	132	2.1e-06

Protein name Locus Name Acc#

conserved hypothetical protein pir:F75328 F75328

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648876_f2_100	4082	9304	237	714		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24820300_c2_241	4083	9305	200	603	122	1.4e-05

Protein name _____ Locus Name _____ Acc# _____

sp:XERC_SALTY P55888

Description

INTEGRASE/RECOMBINASE XERC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25429715_c3_323	4084	9306	546	1641	935	5.8e-112

Protein name _____ Locus Name _____ Acc# _____

helicase gp:RNDNAB Y13813

Description

Rhodothermus marinus dnaB gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25601662_c1_189	4085	9307	105	318		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26574061_f2_106	4086	9308	244	735	472	8.5e-45

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sanA protein	pir:D75549	D75549

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26594082_c1_222	4087	9309	192	579	559	5.1e-54

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
Na-translocating NADH-quinone reductase, Nqr5 subunit	pir:A72399	A72399

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26744012_c1_200	4088	9310	943	2832	2616	5.4e-272

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:UVRA_BACSU	034863

Description

EXCINUCLEASE ABC SUBUNIT A

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26758427_c3_321	4089	9311	202	609	555	1.4e-53

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
Na-translocating NADH-quinone reductase, Nqr4 subunit	pir:H72398	H72398

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2944087_c1_203	4090	9312	115	348	225	1.3e-18

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein SCE20.33c.	gp:SCE20	AL136058

Description

Streptomyces coelicolor cosmid E20.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3025037_c3_287	4091	9313	705	2118	220	5.5e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
site-specific recombinase	gp:D86934	D86934

Description

Staphylococcus aureus genes, mec region, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.3.39.7127_c2_254.....	4092	9314	116	351		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34.022187_c2_272.....	4093	9315	334	1005	766	5.9e-76

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Na-translocating NADH-quinone reductase, Nqr2 subunit	pir:F72398	F72398
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34179712_f3_154	4094	9316	682	2049	1936	6.2e-200

Protein name Locus Name Acc#

sp:UVRB_BACSU

Description

EXCINUCLEASE ABC SUBUNIT B (DINA PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35344626_c1_201	4095	9317	176	531	355	2.1e-32

Protein name Locus Name Acc#

sp:EBSC_ENTFA P36922

Description

EBSC PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36129012_c2_239.....	4096	9318	275	828	312	7.6e-28

Protein name Locus Name Acc#

sp:YBHR_ECOLI P75774

Description

HYPOTHETICAL 41.6 KD PROTEIN IN MOAE-RHLE INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36350812_f1_25.....	4097	9319	62	189		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3940668_f1_45	4098	9320	657	1974	237	8.1e-32

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein ylbK	pir:H69874	H69874

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3945187_E3_137	4099	9321	542	1629	1569	4.8e-161

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:PYRG_BACSU	P13242

Description

CTP SYNTHASE, (UTP--AMMONIA LIGASE) (CTP SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
39453.01_E3_319	4100	9322	293	882	231	2.9e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YDGM_ECOLI	P77223

Description

PUTATIVE FERREDOXIN-LIKE PROTEIN IN ADD-NTH INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
39642_E3_327	4101	9323	196	591	841	6.7e-84

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
dTDP-6-deoxy-D-glucose-3,5 epimerase	gp:AF048749	AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4069800_c2_246	4102	9324	81	246	100	2.2e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:RPC_BPPHI	

Description

IMMUNITY REPRESSOR PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
424002_f3_165	4103	9325	180	543	178	4.7e-13

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
alanine--tRNA ligase,	pir:E72216	E72216

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4.3.28.3.8.0_c2_282.....	4104	9326	298	897	1398	6.3e-143

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glucose-1-phosphate thymidyl transferase	gp:AF048749	AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4.4.5.5.0.0.0_c1_223.....	4105	9327	364	1095	864	2.4e-86

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:GALE_BACSU	P55180

Description

GALACTOSE 4-EPIMERASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4507781_f2_73	4106	9328	277	834	322	6.6e-29

Protein name	Locus Name	Acc#
	sp:YABH_BACSU	P37550

Description

HYPOTHETICAL 31.7 KD PROTEIN IN SSPF-PURR INTERGENIC REGION (ORF1)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4865687_f3_150	4107	9329	598	1797	156	2.2e-08

Protein name	Locus Name	Acc#
cell wall-binding protein homolog yoch	pir:E69901	E69901

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
48.76.6.82...c3...320.....	4108	9330	452	1359	986	2.9e-99

Protein name	Locus Name	Acc#
hypothetical protein TM0244	pir:E72398	E72398

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5.0.95.262_f3_129.....	4109	9331	423	1272		

Protein name	Locus Name	Acc#
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6027187_c1_220	4110	9332	279	840	221	3.3e-18

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YDGP_ECOLI	P77285

Description

HYPOTHETICAL 21.9 KD PROTEIN IN ADD-NTH INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
788125_f3_157	4111	9333	548	1647	122	0.00083

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ORF MSV198 MTG motif gene family protein	gp:AF063866	AF063866

Description

Melanoplus sanguinipes entomopoxvirus, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9.11251_c2_253.....	4112	9334	275	828	155	6.0e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein aq_1273	pir:C70410	C70410

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9.6.8.0_f3_153.....	4113	9335	71	216		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

<u>NO-HIT</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9865837_c3_326	4114	9336	177	534	233	1.8e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF048749	AF048749

<u>Description</u>
Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9921876_c3_295	4115	9337	161	486		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

<u>Description</u>
NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9932642_c1_183.....	4116	9338	106	321	92	0.00016

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

<u>Description</u>
Escherichia coli genomic DNA. (17.6 - 18.0 min).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11131528_c2_62.....	4117	9339	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

<u>Description</u>
NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11133437_f1_3	4118	9340	1168	3507	480	6.8e-42

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (RagA)	gp:PGI130872	AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11719042_f1_1	4119	9341	810	2433	1607	4.5e-165

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable polyribonucleotide nucleotidyltransferase (pnp)	pir:C71269	C71269

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13869.003_f3_31	4120	9342	538	1617	135	2.9e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
cell surface antigen-like protein A29L	pir:T17519	T17519

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14650277_f1_7	4121	9343	253	762		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
26364040_f1_5	4122	9344	86	261		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3.9.0.7.6.8.7_f3_28.....	4123	9345	313	942	115	0.00025

Protein name Locus Name Acc#
transmembrane sensor gp:AF051691 AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4104632_c2_56.....	4124	9346	374	1125	974	5.4e-98

Protein name Locus Name Acc#
butyrate kinase gp:AB016775 AB016775

Description

Clostridium perfringens DNA for butyrate kinase and hydrogenase, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4.3.0.3.26.2_f2_13.....	4125	9347	189	570	196	1.5e-15

Protein name Locus Name Acc#
RNA polymerase sigma factor SigZ-like protein gp:AF137263 AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4305337_f1_4	4126	9348	542	1629		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4765625_c2_73	4127	9349	250	750		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4820378_c2_61	4128	9350	107	324		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5438187_c1_38	4129	9351	317	954	476	3.2e-45

Protein name _____ Locus Name _____ Acc# _____

sp:PTB_CLOAB Q05624

Description

PHOSPHATE BUTYRYLTRANSFERASE, (PHOSPHOTRANSBUTYRYLASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9923505_f1_6	4130	9352	548	1647		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15834557_f1_1	4131	9353	88	267		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
831550_f1_2	4132	9354	388	1164	452	1.4e-41

Protein name Locus Name Acc#
115K outer membrane protein precursor: SusC
protein

pir:JC6027 JC6027

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1959377_f2_2	4133	9355	71	216	93	0.0021

Protein name Locus Name Acc#
maturase-like protein gp:CPESPSBC AJ222583

Description

Euglena spirogyra chloroplast partial psbC gene & complete internal mat2 gene.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24736386_c3_3	4134	9356	62	189		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14241518_c1_6.3	4135	9357	79	240	116	4.5e-07

Protein name Locus Name Acc#

iron(II) transport protein A pir:C72423 C72423

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15017517_f3_3.7	4136	9358	790	2373	912	2.0e-91

Protein name Locus Name Acc#

sp:PBPC_ECOLI P76577

Description

BIFUNCTIONAL PENICILLIN-BINDING PROTEIN 1C PRECURSOR (PBP-1C)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
19692186_f1_3	4137	9359	442	1329	391	1.1e-43

Protein name Locus Name Acc#

cell cycle protein homolog mesJ pir:T31465 T31465

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24067651_f1_15	4138	9360	182	549	137	2.7e-09

Protein name Locus Name Acc#

vsrD protein pir:I40540 I40540

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31803882_f2_28	4139	9361	350	1053	635	4.5e-62

Protein name Locus Name Acc#

conserved hypothetical protein pir:H72370 H72370

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32112785_c3_93	4140	9362	93	282		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
32228163_c1_64	4141	9363	299	897	371	1.7e-40

Protein name Locus Name Acc#

sp:FE0B_METJA Q57986

Description

FERROUS IRON TRANSPORT PROTEIN B HOMOLOG

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33785957_f1_14	4142	9364	208	627		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34183437_f2_29	4143	9365	482	1449	751	2.3e-74

Protein name Locus Name Acc#

Na+/H⁺ antiporter homolog yheL pir:D69829 D69829

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4376056_c1_61	4144	9366	63	192		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4423751_f3_3.8	4145	9367	394	1185	572	2.1e-55

Protein name Locus Name Acc#

antibiotic resistance protein homolog ydeR pir:D69779 D69779

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
648382_f1_4	4146	9368	1870	5613	644	1.5e-60

Protein name Locus Name Acc#

hypothetical protein b2520 pir:G65028 G65028

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10603135_f1_6	4147	9369	161	486	162	6.0e-12

Protein name Locus Name Acc#

hypothetical protein CT276 pir:A71535 A71535

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1179767_f1_7	4148	9370	421	1266		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1251313_c1_26	4149	9371	386	1161	1228	6.5e-125

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:SYW_CLOLO	Q46127

Description

(TRPRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20975051_f1_1	4150	9372	399	1200	396	9.6e-37

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive 42kD antigen PG33	gp:AF175715	AF175715

Description

Porphyromonas gingivalis strain W50 immunoreactive 42kD antigenPG33 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23595253_c1_22	4151	9373	62	189		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24494037_f3_15	4152	9374	304	915		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25516062_f2_10	4153	9375	529	1587	220	1.1e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunogenic 75 kDa protein PG4	gp:AF145800	AF145800

Description

Porphyromonas gingivalis strain W50 immunogenic 75 kDa protein PG4 gene, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30210933_f3_13	4154	9376	332	999	144	4.2e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transposase	gp:AF038866	AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33242837_f2_9	4155	9377	202	609		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4718936_f3_12	4156	9378	1081	3246	3056	0.0

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:PYR1_DICDI	P20054

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7140652_c3_50	4157	9379	112	339	82	0.032

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
EntT	gp:AF099088	AF099088

Description

Enterococcus faecium enterocin A (entA), EntI (entI), EntF (entF), EntK (entK), EntR (entR), bacteriocin-like protein, EntT (entT), EntD (entD), and protease IV homolog genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10741300_f3_30	4158	9380	191	576		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
NO-HIT		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1210910_f2_18.....	4159	9381	389	1170	252	8.5e-29

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
proline dipeptidase	pir:D75419	D75419

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
135050_f3_22.....	4160	9382	69	210		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
NO-HIT		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14651386_f3_29	4161	9383	471	1416	2343	4.6e-243

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:DHE4_BACFR	P94316

Description

(NAD(P)H-DEPENDENT GLUTAMATE DEHYDROGENASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24251553_c2_40	4162	9384	248	747		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24661587_c2_41	4163	9385	201	606		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24895037_c2_39	4164	9386	994	2985	152	8.9e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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probable phosphoenolpyruvate synthase APE0026 pir:E72754 E72754

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26288137_f1_7	4165	9387	81	246	114	1.2e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:PPCE_HUMAN	P48147

Description

(PE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3959800_c3_48	4166	9388	274	825		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16493766_c1_41.....	4167	9389	104	315		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20510052_f3_39.....	4168	9390	63	192		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23627302_f3_40	4169	9391	336	1011	117	0.00030

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transmembrane sensor	gp:AF051691	AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor (fiuL), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24354562_c3_66	4170	9392	515	1548		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24642186_c2_55.....	4171	9393	545	1638	156	3.2e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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unknown	gp:U96771	U96771
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Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24736386_c2_48.....	4172	9394	62	189		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26376562_c2_54	4173	9395	452	1359	477	2.9e-44

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29462512_f1_12	4174	9396	201	606	182	4.5e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
RNA polymerase sigma factor SigZ-like protein	gp:AF137263	AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-likeprotein, fucose gene cluster, and RNA polymerase sigma factorSigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34171886_c2_51	4175	9397	583	1752	110	1.2e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:U96771	U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknowngenes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36442805_c1_43	4176	9398	1128	3387	561	2.1e-86

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (RagA)	gp:PGI130872	AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3929183_c1_47	4177	9399	496	1491		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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331550_c1_46.....	4178	9400	648	1947	588	3.1e-56
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027
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<u>Description</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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331550_c3_61.....	4179	9401	1140	3423	801	5.2e-88
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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receptor antigen (RagA)	gp:PGI130872	AJ130872
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<u>Description</u>

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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990937_c1_45.....	4180	9402	591	1776	121	0.00017
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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outer membrane protein	gp:BNROMPB	L77614
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<u>Description</u>

Bacteroides thetaiotaomicron outer membrane protein (susD) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1208550_f2_43	4181	9403	169	510		

Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12947287_f3_65.....	4182	9404	87	264		

Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13869003_f1_15.....	4183	9405	161	486	215	1.4e-17

Protein name Locus Name

Acc#

unknown gp:AF048749 AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14478901_c2_102.....	4184	9406	77	234		

Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15103800_f1_19	4185	9407	94	285	78	0.018

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
response regulator	gp:AF130997	AF130997

Description

Enterococcus faecium strain BM4339 vanD glycopeptide resistance gene cluster, complete sequence.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15822833_f2_21	4186	9408	76	231	198	5.1e-15

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein yisQ	pir:H69837	H69837

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
166.01633_c2_120.....	4187	9409	85	258		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
166.03427_f2_40.....	4188	9410	402	1209	1820	1.2e-187

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
UDP-ManNAc dehydrogenase	gp:AF125164	AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.
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ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
16832885_c2_101	4189	9411	431	1296	1723	2.3e-177

Protein name	Locus Name	Acc#
hypothetical protein	pir:JQ1020	JQ1020

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
20782802_f3_58	4190	9412	81	246		

Protein name	Locus Name	Acc#
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
21672181_c3_137	4191	9413	278	837		

Protein name	Locus Name	Acc#
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22469452_f1_14	4192	9414	174	525	174	3.2e-13

Protein name	Locus Name	Acc#
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unknown	gp:AF048749	AF048749
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Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22657551_c1_94	4193	9415	565	1698	539	7.9e-58

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
long-chain-fatty-acid CoA ligase	pir:D70386	D70386

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22658450_f2_46	4194	9416	72	219	156	2.7e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
arylsulfotransferase	gp:AF126201	AF126201

Description

Pseudomonas putida strain S-313 sulfate ester desulfurization gene locus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22736336_c2_99	4195	9417	103	312		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_c3_125	4196	9418	83	252	64	0.031

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:SPRC_XENLA	P36378
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Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22899000_f1_17	4197	9419	114	345	59	0.0024

Protein name	Locus Name	Acc#
retinoid X receptor alpha homolog	gp:UPU31832	U31832

Description
Uca pugilator retinoid X receptor alpha homolog mRNA, DNA binding domain region, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24035212_c2_110	4198	9420	129	390		

Protein name	Locus Name	Acc#

Description
NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
242427.00...c3...14.0.....	4199	9421	364	1095	569	6.8e-86

Protein name	Locus Name	Acc#
GDP-L-fucose pathway enzyme	gp:AB008676	AB008676

Description
Escherichia coli 0157 DNA, map position at 46 min., complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
248065.01...c1...95.....	4200	9422	386	1161	153	9.9e-08

Protein name	Locus Name	Acc#
probable PPE protein	pir:D70604	D70604

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2547261_f2_37	4201	9423	83	252		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
259.8842_f1_18	4202	9424	69	210	57	0.041

Protein name Locus Name Acc#

gp:F23A5 AC011713

Description

Arabidopsis thaliana chromosome 1 BAC F23A5 sequence, complete sequence.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2.742.755_f2_47	4203	9425	63	192		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
2.96.938.77_f2_41	4204	9426	390	1173	1608	3.5e-165

Protein name Locus Name Acc#

UDP-GlcNAc 2-epimerase gp:AF125164 AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31444127_f3_51	4205	9427	673	2022	1578	5.3e-162

Protein name Locus Name Acc#
 fructose-bisphosphatase, pir:C69621 C69621

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3314078_f3_71	4206	9428	133	402	125	3.9e-07

Protein name Locus Name Acc#
 probable lipopolysaccharide O-side chain biosynthesis protein (O-antigen transpoter) pir:F71152 F71152

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34266886_c3_136	4207	9429	122	369		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35166437_f2_39	4208	9430	89	270		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35343753_c1_77	4209	9431	61	186		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36134625_f2_36	4210	9432	296	891	1351	6.0e-138

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glucose-1-phosphate thymidyl transferase	gp:AF048749	AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4469002_f3_50	4211	9433	556	1671	955	5.6e-96

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YIDE_ECOLI	

Description

HYPOTHETICAL 58.9 KD PROTEIN IN GLVC-IBPB INTERGENIC REGION (ORFA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
46.94.052_f3_6.7.....	4212	9434	343	1032	1134	6.0e-115

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
Cap8E	gp:SAU73374	U73374

Description

Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4.7203.27_f3_6.2.....	4213	9435	187	564	792	1.0e-78

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
dTDP-6-deoxy-D-glucose-3,5 epimerase	gp:AF048749	AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4941937_c2_112	4214	9436	374	1125	1219	5.9e-124

Protein name Locus Name Acc#

GDP-mannose dehydratase gp:AF047478

Description

Brucella melitensis strain 16M lipopolysaccharide O side chain biosynthesis gene cluster, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5115927_f2_42	4215	9437	364	1095	475	4.1e-45

Protein name Locus Name Acc#

pleiotropic regulatory protein DegT pir:D69025 D69025

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
58.7.81.76_f3_6.8	4216	9438	83	252	76	0.048

Protein name Locus Name Acc#

reverse transcriptase like protein 1, pir:S58503 S58503
intron-encoded

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7.0.6.2.75.0_f2_44	4217	9439	358	1077	334	3.6e-30

Protein name Locus Name Acc#

aspartate aminotransferase (aspb-like1) pir:D75096 D75096
PAB0774

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7314165_f1_11	4218	9440	360	1083	407	6.5e-38

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YA38_HAEIN	P44099

Description

HYPOTHETICAL PROTEIN H11038

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
828957_f3_64	4219	9441	83	252		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10.73.7.8.01_c3_238.....	4220	9442	471	1416	718	7.2e-71

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable oxidoreductase	gp:SCF11	AL132662

Description

Streptomyces coelicolor cosmid F11.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11.8.7.7.138_c2_215.....	4221	9443	319	960	372	3.3e-34

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
shikimate 5-dehydrogenase	pir:F70377	F70377

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11963262_c3_239	4222	9444	263	792	334	3.6e-30

Protein name Locus Name Acc#
 conserved hypothetical protein pir:G72409 G72409
Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1250.76.91_c2_217	4223	9445	274	825	478	2.0e-45

Protein name Locus Name Acc#
 temA protein pir:F72311 F72311
Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
125.3.90.91_c2_23.0	4224	9446	862	2589	493	2.9e-46

Protein name Locus Name Acc#
 sp:ALR2_BACSU P94494
Description

PUTATIVE ALANINE RACEMASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15.05.156.2_c1_181	4225	9447	96	291		

Protein name Locus Name Acc#
Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15.6.57.052_c2_211	4226	9448	169	510		

Protein name Locus Name Acc#
Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15829675_f2_57	4227	9449	525	1578	137	2.3e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (RagA)	gp:PGI130872	AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16131877_c2_231	4228	9450	272	819	318	1.7e-31

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical integral membrane protein HP1061	pir:E64652	E64652

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20089042_c2_205	4229	9451	1043	3132	1063	1.2e-194

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
beta-galactosidase	pir:F72283	F72283

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20710888_f3_138	4230	9452	100	303	72	0.043

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glutamine-asparagine rich protein	gp:DDU07817	U07817

Description

Dictyostelium discoideum AX3 glutamine-asparagine rich protein gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22147552_c2_232	4231	9453	397	1194	268	8.0e-22

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
3-O-acyltransferase, MdmB:midecamycin biosynthesis enzyme	pir:A42719	A42719

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23492786_c2_228	4232	9454	85	258		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23632187_c1_184	4233	9455	262	789	536	1.4e-51

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:LPXA_ECOLI

Description

(EC 2.3.1.129) (UDP-N-ACETYLGLUCOSAMINE ACYLTRANSFERASE)
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23712776_c2_218	4234	9456	389	1170	177	1.1e-23

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:PUR5_METJA	Q57656
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Description

(AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE)
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23850828_c3_254	4235	9457	86	261		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23867302_c2_222	4236	9458	230	693		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24038577_c2_219	4237	9459	370	1113	899	4.8e-90

Protein name Locus Name Acc#

sp:RF1_COXBU P47849

Description

PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24119033_c2_227	4238	9460	130	393		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24223382_c2_206	4239	9461	368	1107	566	9.2e-55
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein slrl880	pir:S77134	S77134
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24299131_c3_257.....	4240	9462	72	219	70	0.033
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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ribosomal protein L20	pir:A75326	A75326
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24391561_c3_248.....	4241	9463	548	1647	395	1.2e-36
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:YUAG_BACSU	032076
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Description

HYPOTHETICAL 56.0 KD PROTEIN IN GLGB-GBSB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24408457_c1_198.....	4242	9464	1180	3543	535	7.0e-59
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein sll1582	pir:S75309	S75309
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24634681_c3_256	4243	9465	462	1389	382	2.7e-44

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:LPXC_HAEIN	P45070

Description

(EC 3.5.1.-)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24640752_f2_45	4244	9466	417	1254		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
246.51.553_c2_22.0.....	4245	9467	248	747	404	1.4e-37

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
OMP decarboxylase-orotate phosphoribosyl transferase,	pir:T30520	T30520

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
246.953.02_c3_24.9.....	4246	9468	251	756	465	4.7e-44

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ubiquinone/menaquinone biosynthesis methyltransferase	pir:F75277	F75277

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24735830_c3_258	4247	9469	395	1188		

Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24801442_f2_44	4248	9470	76	231	90	0.0023

Protein name Locus Name

Acc#

probable glycosyl hydrolase pir:T36467 T36467

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26211057_f1_36	4249	9471	601	1806	91	0.017

Protein name Locus Name

Acc#

polygalacturonase precursor pir:S57806 S57806

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26361438_f2_82	4250	9472	226	681		

Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29344691_f3_110	4251	9473	703	2112	255	8.9e-21

Protein name Locus Name

Acc#

histidine kinase gp:SPAJ6393

AJ006393

Description

Streptococcus pneumoniae rr03 and hk03 genes; two component system03.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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31520840_f2_95	4252	9474	80	240		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3.323.58.8.0_f2_55	4253	9475	64	195		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3.3.6.12.7.6.2_f2_81	4254	9476	318	957	204	5.2e-16
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein aq_246	pir:E70322	E70322
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<u>Description</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3.4.1.7.3.1.7.5_c2_214	4255	9477	318	957	611	1.6e-59
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp: PUR7_ARATH	P38025
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<u>Description</u>

(EC 6.3.2.6) (SAICAR SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3.4.5.4.6.9.4.2_f2_80	4256	9478	399	1200	195	7.7e-15
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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conserved hypothetical protein	pir:C72361	C72361
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<u>Description</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35396062_f1_14	4257	9479	79	240		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35401883_f1_43	4258	9480	147	444		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36523452_c2_216	4259	9481	316	951	327	2.0e-29

Protein name Locus Name Acc#

sp:YQKD_BACSU P54567

Description

HYPOTHETICAL 34.6 KD PROTEIN IN GLNO-ANSR INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3948392_c3_255	4260	9482	349	1050	577	6.3e-56

Protein name Locus Name Acc#

sp:LPXD_RICRI P32202

Description

(EC 2.3.1.-) (FIRA PROTEIN) (RIFAMPICIN RESISTANCE PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3956556_c2_223	4261	9483	304	915	525	2.0e-50

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
trNA isopentenylpyrophosphate transferase miaA	pir:G69657	G69657

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
424042_±1_3.7	4262	9484	264	795	404	1.4e-37

Protein name Locus Name Acc#
sp:TRUA_BACSU P70973

Description

I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
43.51562...c3...250	4263	9485	375	1128	255	1.2e-30

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein	pir:G72311	G72311

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4731562_#3_125	4224	8486	220	62		

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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4767252_c1_174	4265	9487	340	1023	710	5.1e-70

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:BMAJ4829	AJ224829

Description

Bacillus megaterium DSM319 spoIV operon, 5' flanking region, 3' flanking region.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5082512_c3_265	4266	9488	332	999		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6360910_c1_196.....	4267	9489	79	240	155	3.3e-11

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical secreted protein HP0320	pir:H64559	H64559

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7126431_c1_185.....	4268	9490	61	186	72	0.020

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
leech zinc finger protein	gp:HTDNALZF1	X91396

Description

H.triserialis Lzf1 gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
85882_f2_56	4269	9491	135	408	147	2.3e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:MECI_STAEP	P26598

Description

METHICILLIN RESISTANCE REGULATORY PROTEIN MECI

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
992787_c2_221	4270	9492	437	1314	498	1.5e-47

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YWFO_BACSU	P39651

Description

HYPOTHETICAL 51.0 KD PROTEIN IN PTA 3'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14922291_c3_55.....	4271	9493	287	864		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22079700_f2_11.....	4272	9494	174	525	362	3.8e-33

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:RODA_ECOLI

Description

ROD SHAPE-DETERMINING PROTEIN RODA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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23495336_c3_52	4273	9495	115	348		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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2350306_c2_42.....	4274	9496	100	303	105	6.6e-06
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Protein name

Locus Name

Acc#

hypothetical protein PH0217	pir:G71244
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G71244

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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23944506_c2_3.9.....	4275	9497	63	192	108	3.2e-06
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Protein name

Locus Name

Acc#

hypothetical protein PH0219	pir:A71245
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A71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24417061_c1_3.3.....	4276	9498	362	1089	389	5.3e-36
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Protein name

Locus Name

Acc#

sp:METF_AQUAE

O67422

Description

5,10-METHYLENETETRAHYDROFOLATE REDUCTASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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282708_c3_4.5.....	4277	9499	60	183		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5332506_c2_38	4278	9500	95	288	73	0.034

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PH0220	pir:B71245	B71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.7.9.6.7...c2_43.....	4279	9501	492	1479	418	4.5e-39

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YAAT_BACSU	P37541

Description

HYPOTHETICAL 31.2 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9.6.5.8..c1_34.....	4280	9502	370	1113	168	1.1e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
DNA polymerase III gamma subunit	pir:A70460	A70460

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1.0.8.3.8.9.0.5..c1_26.....	4281	9503	97	294		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11197928_f1_1	4282	9504	828	2487	649	4.5e-112

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:BGLS_AGRTU	P27034

Description

GLUCOSIDE GLUCOHYDROLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12698552_c3_72	4283	9505	325	978	398	5.9e-37

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:MMSR_PSEAE	P28809

Description

MMSAB OPERON REGULATORY PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19944466_f1_9.....	4284	9506	348	1047		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2031705_f1_2.....	4285	9507	482	1449	847	1.5e-84

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
L-arabinose transport (permease) araE	pir:F69587	F69587

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24651537_f2_14	4286	9508	1102	3309	2097	5.4e-217

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YPHG_ECOLI	P76585

Description

HYPOTHETICAL 127.3 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34069436_f1_8	4287	9509	940	2823	261	2.5e-18

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
beta-galactosidase	gp:AF055482	AF055482

Description

Thermotoga neapolitana galactose utilization operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15.7.8.9.0.8....c2...51.....	4288	9510	224	675	179	9.5e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
RNA polymerase sigma factor SigZ-like protein	gp:AF137263	AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16.13.14.3.7_f2_20.....	4289	9511	439	1320	118	0.0015

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
BcDNA.GH11973	gp:AF145671	AF145671

Description

Drosophila melanogaster clone GH11973 BcDNA.GH11973 (BcDNA.GH11973)mRNA, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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20895303_f2_21	4290	9512	1227	3684		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>		
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NO-HIT		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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212752_c3_6.9.....	4291	9513	814	2445	518	1.2e-46
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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receptor antigen (RagA)	gp:PGI130872	AJ130872
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<u>Description</u>		
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Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24335781_f3_25.....	4292	9514	140	423	77	0.0064
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:NOLP_RHILP	P23717
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<u>Description</u>		
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NODULATION PROTEIN NOLP		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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25494062_c2_5.0.....	4293	9515	84	255		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>		
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NO-HIT		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>				
26594067_c1_39	4294	9516	320	963	155	1.2e-08				
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>				
transmembrane sensor					gp:AF051691	AF051691				
<u>Description</u>										
Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor(fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.										

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>				
4103377_f3_30	4295	9517	119	360						
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>				
NO-HIT										
<u>Description</u>										
NO-HIT										
<u>Description</u>										
Bacteroides fragilis nanH gene for neuraminidase, complete cds.										

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>				
148.7.6.3.0.0_c2_90	4297	9519	532	1599	139	6.7e-08				
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>				
unknown					gp:U96771	U96771				
<u>Description</u>										
Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.										

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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16267638_c2_67	4298	9520	93	282		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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21595663_f3_39.....	4299	9521	1083	3252	519	4.8e-84
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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22861562_f2_28.....	4300	9522	861	2586	1101	1.9e-111
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein TM1624	pir:H72228	H72228
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24256587_f2_17.....	4301	9523	549	1650	125	1.5e-06
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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unknown	gp:U96771	U96771
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Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24259683_f2_27	4302	9524	691	2076	331	8.1e-35

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sialic-acid O-acetylesterase	gp:MMU40408	U40408

Description

Mus musculus lysosomal sialic acid O-acetylesterase mRNA, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24415877_f3_33	4303	9525	521	1566	107	1.2e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:U96771	U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknowngenes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24429.036..c1..51.....	4304	9526	64	195		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
246408.92..f2..23.....	4305	9527	673	2022		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24648937_f3_41	4306	9528	209	630	126	2.6e-06
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:PA1B_RAT	035264
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Description

ACTIVATING FACTOR ACETYLHYDROLASE ALPHA 2 SUBUNIT) (PAF-AH ALPHA 2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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2772937_c2_89	4307	9529	1093	3282	528	3.0e-89
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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33243818_f2_13.....	4308	9530	434	1305	740	1.2e-84
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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alpha-L-fucosidase, I precursor, tissue:alpha-L-fucosidase I:alpha-L-fucoside fucohydrolase	pir:HWHUFA
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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34416427_f1_11.....	4309	9531	672	2019	310	9.2e-26
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:HEXA_PORGI	P49008
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Description

(BETA-NAHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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35351583_c3_124	4310	9532	71	216		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>		
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NO-HIT		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4140927_f3_43.....	4311	9533	518	1557	1139	1.8e-115
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:HEXA_PORGI	P49008
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<u>Description</u>		
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(BETA-NAHASE)		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4484687_f3_32.....	4312	9534	529	1590	119	1.8e-06
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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unknown	gp:U96771	U96771
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<u>Description</u>		
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Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5109392_c1_64.....	4313	9535	173	522		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>		
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NO-HIT		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
781932_f1_4	4314	9536	1118	3357	463	5.9e-82

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (RagA)	gp:PGI130872	AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
781932_f2_16	4315	9537	1102	3309	526	5.1e-83

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor: SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
781932_f3_31.....	4316	9538	1120	3363	529	2.6e-79

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor: SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
859438_c3_108.....	4317	9539	85	258		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1206500_f1_15	4318	9540	385	1158	465	4.7e-44
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
probable nagA protein					pir:C70845	C70845
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1272677_f3_45	4319	9541	398	1197	384	1.8e-35
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein b1325					pir:H64881	H64881
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1465625_f1_8	4320	9542	451	1356	479	2.7e-48
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein					pir:A72430	A72430
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1959437_f1_18	4321	9543	70	213		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
NO-HIT						
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2147656_f2_25	4322	9544	406	1221	225	3.8e-18
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
polysugar degrading enzyme homolog ykfC					pir:A69856	A69856
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2350306_c1_62	4323	9545	100	303	111	1.5e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PH0217	pir:G71244	G71244

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24407827_f3_50	4324	9546	521	1566	600	2.3e-58

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:HTRA_ECOLI	

Description

PROTEASE DO PRECURSOR,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24642211_f2_30	4325	9547	135	408		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24665887_f2_20	4326	9548	230	693	287	3.4e-25

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
phosphate transport system regulator PhoU	pir:G72275	G72275

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25977212_f1_3	4327	9549	69	210		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26367177_c3_110	4328	9550	439	1320	253	2.2e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sensory protein kinase	pir:T30222	T30222

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
293.1525_f2_31.....	4329	9551	394	1185	192	3.3e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
clostripain-related protein	pir:B72351	B72351

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.0494212_f3_51.....	4330	9552	95	288		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
NO-HIT		

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.3.3.9.7.186_f1_10.....	4331	9553	301	906	933	1.2e-93

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
SigA	gp:CTU67718	U67718

Description

Chlorobium tepidum SigA (sigA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33398377_f3_43	4332	9554	205	618	384	1.8e-35

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:RISA_BACSU	

Description

RIBOFLAVIN SYNTHASE ALPHA CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33863876_c2_96	4333	9555	527	1584		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.5.3.6.6.25....f2_3.7.....	4334	9556	128	387		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.6.4.3.0.3.9.3....f3_4.4.....	4335	9557	189	570	141	4.2e-15

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:YDGI_BACSU	P96707
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Description

PUTATIVE NAD(P)H NITROREDUCTASE YDGI,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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36525157_f2_19	4336	9558	125	378	496	2.4e-47
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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phosphate transport ATP binding protein	pir:G70390	G70390
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3.9.0.826_c1_76.....	4337	9559	451	1356	382	2.9e-35
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:RBN_HAEIN	P44608
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Description

RIBONUCLEASE BN, (RNASE BN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4.8.8.1450_c3_112.....	4338	9560	157	474		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5.6.7.4.0.6.2_c3_113.....	4339	9561	283	852		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
78158_c1_67	4340	9562	236	711	383	2.3e-35
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
				sp:PHOP_BACSU		P13792

Description

PHOP

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15103800_c3_56	4341	9563	94	285	78	0.018
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
response regulator				gp:AF130997		AF130997

Description

Enterococcus faecium strain BM4339 vanD glycopeptide resistance gene cluster, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
157263_c3_59.....	4342	9564	385	1158		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c1_38.....	4343	9565	431	1296	1723	2.3e-177
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
hypothetical protein				pir:JQ1020		JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_E3_33	4344	9566	208	624	710	5.1e-70

Protein name Locus Name Acc#

hypothetical protein pir:JQ1020 JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
18.8.96.7_E3_26.....	4345	9567	91	276		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20.08.7.753_c3_6.3.....	4346	9568	317	954	1426	6.8e-146

Protein name Locus Name Acc#

putative UDP-GlcNAc:undecaprenylphosphate gp:AF048749 AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20.4.093.7_c2_5.2.....	4347	9569	253	762	207	1.0e-16

Protein name Locus Name Acc#

putative glycosyl transferase gp:LPN7311 AJ007311

Description

Legionella pneumophila serogroup 1 lipopolysaccharide biosynthesis gene cluster.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20594161_c3_61	4348	9570	91	276		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22658450_c1_34.....	4349	9571	72	219	156	2.7e-10

Protein name Locus Name Acc#

arylsulfotransferase gp:AF126201 AF126201

Description

Pseudomonas putida strain S-313 sulfate ester desulfurization gene locus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_c2_49.....	4350	9572	83	252	64	0.031

Protein name Locus Name Acc#

sp:SPRC_XENLA P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_t1_15.....	4351	9573	83	252	64	0.031

Protein name Locus Name Acc#

sp:SPRC_XENLA P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24238263_f1_7	4352	9574	129	390		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26.212.76.2_c2_48.....	4353	9575	350	1053	123	9.7e-08

Protein name Locus Name Acc#

Cap5J gp:SAU81973 U81973

Description

Staphylococcus aureus capsule gene cluster Cap5A through Cap5Pgenes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
27.42.755_c1_35.....	4354	9576	63	192		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32.056.392_c1_39.....	4355	9577	69	210	85	0.010

Protein name Locus Name Acc#

hypothetical protein, 57.8 kd gp:POL245436

Description

Pseudomonas putida OCT plasmid alk genes cluster and flanking DNA, strain TF4-1L.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3314078_c2_46	4356	9578	470	1413	252	6.0e-19
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
probable lipopolysaccharide O-side chain biosynthesis protein (O-antigen transpoter)				pir:F71152	F71152	

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.346.0.952_c2_54.....	4357	9579	171	516	95	9.5e-05
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
sp:DBH5_RHILE				sp:DBH5_RHILE	P02348	

Description

DNA-BINDING PROTEIN HRL53						
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.5.9.7.0.967_f3_27.....	4358	9580	62	189	71	0.026
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
sp:HIPB_ECOLI				sp:HIPB_ECOLI	P23873	

Description

HIPB PROTEIN						
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.9.0.7.151_f1_11.....	4359	9581	80	243		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	

Description

NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3945302_f1_8	4360	9582	60	183		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>		
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NO-HIT		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4103387_c1_36.....	4361	9583	305	918	204	2.1e-16
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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probable rhamnosyltransferase	pir:H75596	H75596
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<u>Description</u>		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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41293_c3_60.....	4362	9584	87	264		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>		
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NO-HIT		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4176566_c1_40.....	4363	9585	77	234	82	0.023
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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unknown	gp:AF134706	AF134706
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<u>Description</u>		
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Sinorhizobium meliloti insertion sequence ISRm14, complete sequence.	
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4198425_c2_47	4364	9586	327	984	130	1.6e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:AB000222	AB000222

Description

Staphylococcus capitis epr gene , complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4704715_c3_62	4365	9587	338	1017	1447	4.1e-148

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
UDP-glucose-4-epimerase/dTDP-glucose-4,6	gp:AF048749	AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.9.7.0193..f1..1.....	4366	9588	69	210		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.9.7.8.3.8.5..c1..3.7.....	4367	9589	345	1038		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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6725327_c2_51	4368	9590	238	717	296	3.8e-26
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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glycosyltransferase	pir:G75596	G75596
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<u>Description</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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13689660_f3_10	4369	9591	267	804	1330	1.0e-135
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:ISTB_BACFR	Q45120
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<u>Description</u>

INSERTION SEQUENCE IS21-LIKE PUTATIVE ATP-BINDING PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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14272692_f3_8	4370	9592	333	1002	1671	7.4e-172
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:TRA2_BACFR	Q45119
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<u>Description</u>

TRANSPOSSASE FOR INSERTION SEQUENCE ELEMENT IS21-LIKE

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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16299062_f3_11	4371	9593	592	1779		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22460186_F2_6	4372	9594	64	195		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29937943_F2_4	4373	9595	214	645	1109	2.7e-112

Protein name Locus Name Acc#

sp:TRA2_BACFR Q45119

Description

TRANSPOSEASE FOR INSERTION SEQUENCE ELEMENT IS21-LIKE

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.0525762_F2_7	4374	9596	123	372		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1.00385_F1_32	4375	9597	72	219		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12285135_c3_311	4376	9598	752	2259	1461	1.3e-149

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:BIOA_HAEIN	P44426

Description

AMINOTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12688437_c3_302	4377	9599	489	1470	578	4.9e-56

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive 53 KD antigen PG123	gp:AF144641	AF144641

Description

Porphyromonas gingivalis strain W50 immunoreactive 53 KD antigenPG123 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12947777_f2_99.....	4378	9600	190	573		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13828450_f3_154.....	4379	9601	140	423	86	0.019

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:FKBA_ECOLI

Description

(EC 5.2.1.8) (PPIASE) (ROTAMASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13835937_f2_100	4380	9602	454	1365	789	2.2e-78

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
dihydrolipoamide dehydrogenase, :2-oxoglutarate dehydrogenase complex chain E3:acetoacetyl dehydrogenase complex	pir:140794	I40794
<u>Description</u>		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14095406_c1_182	4381	9603	140	423		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>		

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14727331_c1_191	4382	9604	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
<u>Description</u>		

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14737507_c2_221	4383	9605	129	390	132	9.2e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein APE1673	pir:E72548	E72548
<u>Description</u>		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15040893_f3_137	4384	9606	1043	3132	729	1.7e-120

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (Raga)	gp:PGI130872	AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_f3_155	4385	9607	200	603	762	1.6e-75

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:JQ1020	JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
175317_c3_292.....	4386	9608	74	225		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
199062_f1_48.....	4387	9609	73	222		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20582930_c3_321	4388	9610	522	1569	814	4.9e-81

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
Salmonella typhimurium transcriptional	gp:STYSTMF1	AF170176

Description

Salmonella typhimurium fragment STMF1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20750302_f1_44	4389	9611	459	1380	445	6.3e-71

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ODB2_BACSU	P37942

Description

CHAIN TRANSACYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
219.710.36_c2_28.2	4390	9612	68	207		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
222.7.7_c1_15.7	4391	9613	289	870	298	2.3e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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gp:AB023064 AB023064

Description

Listeria monocytogenes DNA for DnaK operon, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
22860128_f1_52	4392	9614	83	252	64	0.031

Protein name	Locus Name	Acc#
	sp:SPRC_XENLA	P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23851527_c3_312	4393	9615	405	1218	1026	1.7e-103

Protein name	Locus Name	Acc#
	sp:BIOF_HAEIN	P44422

Description

LIGASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24432030_f2_88.....	4394	9616	563	1692	114	1.2e-06

Protein name	Locus Name	Acc#
unknown	gp:U96771	U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24641932_f1_40.....	4395	9617	555	1668		

Protein name	Locus Name	Acc#
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24644015_c3_296	4396	9618	152	459	204	7.4e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
prolidase	gp:AB014613	AB014613

Description

Aureobacterium esteraromaticum gene for prolidase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24645252_f3_123	4397	9619	441	1326	476	3.2e-45

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive 50kD antigen PG53	gp:AF175720	AF175720

Description

Porphyromonas gingivalis strain W50 immunoreactive 50kD antigenPG53 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648407_c3_301.....	4398	9620	199	600		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24666005_c3_316.....	4399	9621	68	207	49	0.036

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein A556L	pir:T18058	T18058

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25448566_f1_18	4400	9622	267	804	564	1.5e-54

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YF08_METJA	Q58903

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ1508

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
255313_c1_163	4401	9623	74	225		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26.3.6.9.0.0.6....f2....94.....	4402	9624	515	1548	1829	1.3e-188

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
propionyl-CoA carboxylase	gp:AB007000	AB007000

Description

Myxococcus xanthus MxppcB gene for propionyl-CoA carboxylase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26.445.31.1....c2....26.3.....	4403	9625	229	690	502	5.6e-48

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:BID2_HAEIN	P45248

Description

2) (DTB SYNTHETASE 2) (DTBS 2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26461542_f2_95	4404	9626	509	1530	1297	3.2e-132

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
acetyl-CoA carboxylase (biotin carboxylase subunit) accC	pir:A69581	A69581

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26594425_f2_69	4405	9627	417	1254	214	5.6e-15

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein aq_294	pir:H70326	H70326

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31281883_f3_134	4406	9628	118	357	110	1.9e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein APE1466	pir:B72626	B72626

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32115637_f1_43	4407	9629	242	729	336	2.2e-30

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:LPLA_MYCPN	P75394

Description

PROBABLE LIPOATE-PROTEIN LIGASE A,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32116703_c2_268	4408	9630	68	207	136	3.4e-09

Protein name Locus Name Acc#

hypothetical protein APE2061 pir:G72510 G72510

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32226550_f3_152	4409	9631	174	525	367	1.1e-33

Protein name Locus Name Acc#

flavodoxin pir:A28670

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32633411_f3_125	4410	9632	810	2433	171	2.0e-09

Protein name Locus Name Acc#

conserved hypothetical protein pir:G72385 G72385

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33218827_c3_300	4411	9633	513	1542		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3370317_f1_38	4412	9634	144	435	154	5.8e-14

Protein name Locus Name Acc#

methylmalonyl-coa decarboxylase gamma chain PAB1771 pir:F75135 F75135

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35367263_c2_266	4413	9635	433	1302		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
357.10811_c1_187	4414	9636	502	1509	468	2.2e-44

Protein name Locus Name Acc#

sp:BIOC_HAEIN P45249

Description

PUTATIVE BIOTIN SYNTHESIS PROTEIN BIOC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.929.091_c1_201	4415	9637	376	1131	256	6.5e-22

Protein name Locus Name Acc#

membrane protein pir:G64590 G64590

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.948.425_f1_3	4416	9638	402	1209	856	1.7e-85

Protein name Locus Name Acc#

aspartate aminotransferase pir:D72220 D72220

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4337882_f3_151	4417	9639	695	2088	1022	4.4e-103

Protein name Locus Name Acc#
probable (pyruvate) oxoisovalerate dehydrogenase alpha and beta fusion pir:G71526 G71526

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4462535_f1_4	4418	9640	438	1317	283	4.4e-23

Protein name Locus Name Acc#
sp:YCFW_ECOLI P75958

Description

HYPOTHETICAL 45.3 KD PROTEIN IN MFD-COBB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4486.037_c3_33.0	4419	9641	415	1248	379	6.1e-35

Protein name Locus Name Acc#
hypothetical protein APE1887 pir:G72575 G72575

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
48.0768.7_c3_30.3	4420	9642	503	1512	941	1.7e-94

Protein name Locus Name Acc#
L-lactate permease (lctP) homolog pir:C70175 C70175

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4953527_f1_51	4421	9643	480	1443	104	1.0e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:PRTT_PORGI	P43158

Description

THIOL PROTEASE/HEMAGGLUTININ PRTT PRECURSOR,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4957582_c2_281	4422	9644	281	846	209	7.8e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:CHAC_SPHHE	Q59288

Description

(CHONDROITIN SULFATE LYASE) (CHONDROITIN AC ELIMINASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5195132_c2_275.....	4423	9645	425	1278	289	4.7e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sensor protein pils	pir:S70528	

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
523587_c3_319.....	4424	9646	434	1305		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

<u>NO-HIT</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
54802_c2_264	4425	9647	456	1371	643	6.4e-63
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
NADH dehydrogenase, :protein slr0851:protein slr0851				pir:S74826	S74826	

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
628465_c1_172	4426	9648	344	1035	369	6.9e-34
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
sp:YJV3_YEAST				sp:YJV3_YEAST	P40896	

Description

HYPOTHETICAL 35.9 KD PROTEIN IN HXT8-CRT1 INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
882912_f1_41	4427	9649	395	1188		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
NO-HIT				NO-HIT		

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
914202_c2_276	4428	9650	390	1173	162	2.9e-09
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
EpsG				gp:AF036485		

Description

Plasmid pNZ4000, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1172330_f1_2	4429	9651	345	1038	1055	1.4e-106

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ketol-acid reductoisomerase	gp:PSP16743	Y16743

Description

Piromyces sp. E2 mRNA for ketol-acid reductoisomerase.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20443775_c1_29	4430	9652	644	1935	717	9.2e-71

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein T18E12.6	pir:T02699	T02699

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23448402_f3_16.....	4431	9653	658	1977		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23478512_f1_1.....	4432	9654	198	597		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24017827_f2_12	4433	9655	247	744	184	2.5e-15

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
palmitoyl-acyl carrier protein thioesterase	gp:AF034266	AF034266

Description

Gossypium hirsutum palmitoyl-acyl carrier protein thioesterase(FatB1) mRNA, partial cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24331376_f1_9	4434	9656	790	2373	2363	3.5e-245

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ACON_GRAVE	P49609

Description

HYDRO-LYASE) (ACONITASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24630192_f2_11.....	4435	9657	153	462	151	8.8e-11

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
acetolactate synthase	pir:E70459	E70459

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4877202_f1_10.....	4436	9658	303	909	867	3.9e-98

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
isocitrate dehydrogenase	gp:BIISOCIT	Y13358

Description

Bacillus israelii isocitrate dehydrogenase gene.
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ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
12509425_f1_8	4437	9659	191	576	639	1.7e-62

Protein name	Locus Name	Acc#
	gp:AB022867	AB022867

Description

Prevotella ruminicola genes for polyA polymerase, D-alanineglycinepermease and cellulase, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13837557_c3_73	4438	9660	123	372	113	9.3e-07

Protein name	Locus Name	Acc#
	gp:MZECWAB	M36913

Description

Z.mays cell wall protein mRNA, 3' end.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14461002_f2_16.....	4439	9661	299	900	264	3.3e-22

Protein name	Locus Name	Acc#
	sp:YEBA_HAEIN	P44693

Description

HYPOTHETICAL PROTEIN HI0409

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
14744002_f2_14.....	4440	9662	184	555	317	2.2e-28

Protein name	Locus Name	Acc#
4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein (thiJ) homolog	pir:D70177	D70177

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860927_f1_7	4441	9663	166	501	362	3.8e-33

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable nucleoside-diphosphate kinase,	pir:C71116	C71116

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24098388_c2_56	4442	9664	310	933	591	2.1e-57

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:PGPUT	X97228

Description

P.gingivalis gpdXJ, put, and yhbG-pg genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26213181_c3_61	4443	9665	257	774	992	6.7e-100

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:JQ1020	JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26759387_f2_17	4444	9666	444	1335		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29480341_c1_44	4445	9667	85	255		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3312913_f3_27	4446	9668	223	672	336	2.2e-30

Protein name Locus Name Acc#

conserved hypothetical protein yacM pir:S66119

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33392202_f2_18	4447	9669	267	804	587	5.5e-57

Protein name Locus Name Acc#

triosephosphate isomerase gp:AF043386 AF043386

Description

Clostridium acetobutylicum glyceraldehyde-3-phosphate dehydrogenase (gap), phosphoglycerate kinase (pgk), and triosephosphate isomerase (tpi) genes, complete cds; and 2,3-bpg-independent phosphoglyceratemutase (pgm-i) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33476625_f2_15	4448	9670	707	2124	1284	7.6e-131

Protein name Locus Name Acc#

sp:RECG_SYNY3 Q55681

Description

ATP-DEPENDENT DNA HELICASE RECG,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34081405_f3_22	4449	9671	88	267	110	1.9e-06

Protein name Locus Name Acc#

hypothetical protein PHS004 pir:F71245 F71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35205387_f3_26	4450	9672	293	882	256	6.5e-22

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:TONB_NEIGO	006432

Description

TONB PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4159587_f3_24	4451	9673	211	636	676	2.0e-66

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
pyridoxal phosphate synthetase	gp:PGPUT	X97228

Description

P.gingivalis gpdxJ, put, and yhbG-pg genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4578461_f1_5.....	4452	9674	149	450	139	1.6e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:TOLR_HAEIN	P43769

Description

TOLR PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5087912_c2_59.....	4453	9675	89	270		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9853312_f3_25	4454	9676	245	738	232	2.3e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	gp:PST243354	AJ243354

Description

Pseudomonas stutzeri hyp1 and comA genes and putative tolQ, exbB, tolR and exbD genes.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10137_c2_279	4455	9677	185	558	537	1.1e-51

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
carbonic anhydrase homolog ytiB	pir:F69993	F69993

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
106.3.2.7.6.8...c3...3.21.....	4456	9678	68	207		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
106.7.5.6.8.0...c2...245.....	4457	9679	74	225		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12600340_f3_137	4458	9680	364	1095		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12676061_f1_4	4459	9681	474	1425		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1353457_f1_34	4460	9682	461	1386	461	1.6e-56

Protein name Locus Name Acc#

AlgI gp:PAU50202 U50202

Description

Pseudomonas aeruginosa alginate gene cluster AlgI (algI), AlgJ(algJ) and AlgF (algF) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13785326_f2_111	4461	9683	68	207		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14541001_f2_82	4462	9684	382	1149	315	3.7e-28

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
thiamin biosynthesis protein homolog	pir:H69260	H69260

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14634500_c2_298	4463	9685	455	1368	153	3.7e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
KIAA1275 protein	gp:AB033101	AB033101

Description

Homo sapiens mRNA for KIAA1275 protein, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14650287_c3_304	4464	9686	540	1623	416	6.4e-67

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
outer membrane protein	gp:BNROMPPB	L77614

Description

Bacteroides thetaiotaomicron outer membrane protein (susD) gene, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14712516_c3_359	4465	9687	133	402		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14954712_f1_49	4466	9688	150	453	125	5.0e-08

Protein name Locus Name Acc#
sp:MEXR_PSEAE P52003

Description

MULTIDRUG RESISTANCE OPERON REPRESSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16101587_f1_50	4467	9689	359	1080	403	1.7e-37

Protein name Locus Name Acc#
sp:EMRA_HAEIN P44928

Description

MULTIDRUG RESISTANCE PROTEIN A HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16.8.3.28.8.5_c2_28.5.....	4468	9690	431	1296	1723	2.3e-177

Protein name Locus Name Acc#
hypothetical protein pir:JQ1020 JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16.9.0.5_f2_7.5.....	4469	9691	64	195		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20015643_c3_312	4470	9692	66	201		

Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20369826_c3_332	4471	9693	190	573	240	3.2e-20

Protein name

Locus Name

Acc#

sp:YM67_ARCFU

028017

Description

(EC 1.---)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20509630_c1_184	4472	9694	954	2865	345	3.3e-28

Protein name

Locus Name

Acc#

alpha-amylase, precursor:protein c0620

pir:S73087

S73087

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22287681_f3_174	4473	9695	402	1209	152	4.0e-10

Protein name

Locus Name

Acc#

thiol:disulfide interchange protein homolog
yneN

pir:E69891

E69891

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>				
22459655_c3_360	4474	9696	337	1014	133	4.7e-06				
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>				
transmembrane sensor					gp:AF051691	AF051691				
<u>Description</u>										
<i>Pseudomonas aeruginosa</i> stress factor A (psfA), ECF sigma factor (fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.										

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22478431_f2_84	4475	9697	397	1194	282	1.1e-23
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
					sp:YRKO_BACSU	P54442
<u>Description</u>						

HYPOTHETICAL 46.4 KD PROTEIN IN BLTR-SPOTTIC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>				
226.8.776.7_f1_19.....	4476	9698	421	1266	770	1.9e-113				
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>				
cytosolic phosphoglycerate kinase 1					gp:AB018410	AB018410				
<u>Description</u>										
<i>Populus nigra</i> PnCytPGK1 mRNA for cytosolic phosphoglycerate kinase1, complete cds.										

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>				
228.6.0128_c3_340.....	4477	9699	83	252	64	0.031				
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>				
					sp:SPRC_XENLA	P36378				
<u>Description</u>										
(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)										

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23554563_F2_81	4478	9700	229	690	493	5.0e-47

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
endonuclease III	pir:B71919	B71919

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23634703_c2_280	4479	9701	69	210	58	0.0059

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ARCD_PSEAE	P18275

Description

ARGININE/ORNITHINE ANTIPORTER

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24000925_c2_301	4480	9702	723	2169	440	4.2e-46

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor: SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24016525_c2_259	4481	9703	343	1032	1174	3.4e-119

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ALF_TREPA	083668

Description

FRUCTOSE-BISPHOSPHATE ALDOLASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24017303_c1_242	4482	9704	677	2034	2862	4.6e-298

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
pullulanase	gp:BTU67061	U67061

Description

Bacteroides thetaiotaomicron pullulanase (pull) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24041626_f3_161	4483	9705	452	1359	141	1.5e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein MTH83	pir:F69210	F69210

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24415877_f3_149	4484	9706	131	396		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24417075_f3_158	4485	9707	167	504	343	4.0e-31

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PH0272	pir:A71452	A71452

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24487937_f1_46	4486	9708	425	1278	153	6.0e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein BB0195	pir:C70124	C70124

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24689717_F3_135	4487	9709	443	1332	422	1.7e-39

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
antibiotic resistance protein homolog ywoG	pir:B70065	B70065

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24695316_E2_76.....	4488	9710	349	1050	788	2.8e-78

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:SYFA_BACSU	

Description

-TRNA LIGASE ALPHA CHAIN) (PHERS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25634375_c2_246.....	4489	9711	97	294		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2595036_c3_358.....	4490	9712	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25978377_F2_85	4491	9713	733	2202	228	1.8e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:Y798_METJA	Q58208

Description

HYPOTHETICAL PROTEIN MJ0798

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26600187_F2_88	4492	9714	508	1527	499	6.4e-51

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:AB019578	AB019578

Description

Microcystis aeruginosa mcyA, mcyB and mcyC genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26756557_f1_28.....	4493	9715	173	522		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29971007_c3_315.....	4494	9716	72	219		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3125006_c2_257	4495	9717	60	183		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31276925_f1_39	4496	9718	285	858		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31854557_c2_247	4497	9719	246	741	503	4.9e-48

Protein name Locus Name Acc#

115K outer membrane protein precursor: SusC protein pir:JC6027 JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31876687_f1_33	4498	9720	97	294	102	1.4e-05

Protein name Locus Name Acc#

acyl carrier protein pir:S28475

S28475

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32620812_F2_108	4499	9721	540	1623	176	4.8e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
VceB	gp:AF012101	AF012101

Description

Vibrio cholerae efflux gene A (vceA) and efflux gene B (vceB) multidrug resistance pump genes, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3377027_c1_213	4500	9722	310	933	135	1.3e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:F72216	F72216

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34414052_c3_3.33.....	4501	9723	175	528	285	5.5e-25

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein aq_2171	pir:D70486	D70486

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.58.2046.1_c3_3.16.....	4502	9724	63	192		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36360000_f2_112	4503	9725	624	1875	121	0.00057

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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unknown	gp:AF013216
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Description

Myxococcus xanthus Dog (dog), isocitrate lyase (icl), Mls (mls),Ufo (ufo), fumarate hydratase (fhy), and proteosome major subunit(clpP) genes, complete cds; and acyl-CoA oxidase (aco) gene,partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
391540_c1_201	4504	9726	61	186		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4094816_f3_164.....	4505	9727	620	1863	1365	2.0e-139

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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neopullulanase	gp:BTU66897	U66897
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Description

Bacteroides thetaiotaomicron neopullulanase (susA) and alpha-glucosidase (susB) genes, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4104062_f1_58.....	4506	9728	88	267	242	2.0e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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probable ribosomal protein L31	pir:T36353	T36353
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4144002_c1_243	4507	9729	190	573	292	1.0e-25

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
RNA polymerase sigma factor SigZ-like protein	gp:AF137263	AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4172012_c1_223	4508	9730	283	852	464	6.0e-44

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
endo-beta-galactosidase	gp:AF083896	AF083896

Description

Flavobacterium keratolyticus endo-beta-galactosidase gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
43.20.313_f2_99.....	4509	9731	520	1563	1634	6.2e-168

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
methylmalonyl-CoA decarboxylase, alpha chain	pir:A49094	A49094

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
43.20.38.7_f2_100.....	4510	9732	146	441	242	2.0e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glutaconyl-CoA decarboxylase gamma subunit	gp:AF030576	AF030576

Description

Acidaminococcus fermentans methylmalonyl-CoA decarboxylase alpha subunit (mmdA) gene, partial cds; and glutaconyl-CoA decarboxylase delta subunit (gcdD), glutaconyl-CoA decarboxylase gamma subunit (gcdC), and glutaconyl-CoA decarboxylase beta subunit (gcdB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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492206_f1_35	4511	9733	352	1059		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4945187_c2_248.....	4512	9734	538	1617	92	0.0019
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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outer membrane protein	gp:BNROMPA	L77615
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<u>Description</u>

Bacteroides thetaiotaomicron outer membrane protein (susE) gene, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5328165_c2_282.....	4513	9735	210	633	336	2.2e-30
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:MAF_BACSU

<u>Description</u>

MAF PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5330267_c2_299.....	4514	9736	200	603	295	4.8e-26
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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crossover junction endodeoxyribonuclease	pir:B72360	B72360
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<u>Description</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5890712_f3_171	4515	9737	118	357		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
59.00682_f1_42	4516	9738	308	927		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
97.72930_f2_116	4517	9739	104	315		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
97.96.942_c2_25.8	4518	9740	363	1092		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
98.47.33.0_f3_16.0	4519	9741	353	1062	966	3.8e-97

Protein name Locus Name Acc#

oxaloacetate decarboxylase, beta subunit pir:B72324 B72324

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13134680_f3_49	4520	9742	194	585	126	5.8e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
beta-galactosidase,	pir:T29434	T29434

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14720382_f1_14	4521	9743	83	252		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14845965_f2_35	4522	9744	250	753	138	1.3e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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M-protein	gp:SEU73162	U73162
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Description

Streptococcus equi M-protein (seM) gene, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15899063_c3_109	4523	9745	81	246		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>					
16604818_c1_71	4524	9746	783	2352	200	4.7e-15					
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>						
colicin I receptor				gp:ECOCIR							
<u>Description</u>											
E.coli colicin I receptor gene, complete cds.											
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>					
17069076_f1_15	4525	9747	253	762	257	5.1e-22					
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>						
				sp:YJJG_ECOLI							
<u>Description</u>											
HYPOTHETICAL 25.3 KD PROTEIN IN RIMI-PRFC INTERGENIC REGION											
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>					
20.784.7.08_f1_1.....	4526	9748	66	201	81	0.021					
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>						
glutamyl-tRNA reductase				gp:AF080069							
<u>Description</u>											
Chlorobium vibrioforme glutamyl-tRNA reductase (hemA) gene, complete cds; and porphobilinogen deaminase (hemC) gene, partial cds.											
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>					
23.5.95.0.55_c3_94.....	4527	9749	722	2169	342	1.1e-41					
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>						
115K outer membrane protein precursor:SusC protein				pir:JC6027	JC6027						
<u>Description</u>											

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24225385_F2_38	4528	9750	73	222		

Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24422505_F1_13	4529	9751	287	864	98	0.0043

Protein name Locus Name

Acc#

hypothetical protein pir:T10699 T10699

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25504687_G2_84	4530	9752	219	660	568	5.7e-55

Protein name Locus Name

Acc#

thymidine kinase gp:AF028720 AF028720

Description

Rhodothermus sp. 'ITI 518' thymidine kinase (tdk) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33439.010_G1_63	4531	9753	947	2844	968	2.3e-97

Protein name Locus Name

Acc#

receptor antigen (Raga) gp:PGI130872 AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34178252_c1_64	4532	9754	537	1614		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.6.018.792..E2..34.....	4533	9755	239	720	568	5.7e-55

Protein name Locus Name Acc#

conserved hypothetical protein pir:D72343 D72343

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.913.937..G3..93.....	4534	9756	507	1524	146	3.9e-14

Protein name Locus Name Acc#

unknown gp:U96771 U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.948412..c1..72.....	4535	9757	418	1257		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4351417_c1_68	4536	9758	394	1185	300	1.4e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable permease perm homolog (perm) RP630	pir:E71668	E71668

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4739778_f2_21	4537	9759	195	588		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
474143_f2_24	4538	9760	543	1632	628	2.8e-95

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
endo-1,4-beta-xylanase,	pir:T30909	T30909

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4976501_f1_9	4539	9761	339	1020	242	2.0e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
regulatory protein pchR-2:protein slr1489:protein slr1489	pir:S74456	S74456

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5964205_f3_58	4540	9762	71	216		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6914125_f3_55	4541	9763	242	729	363	3.0e-33

Protein name	Locus Name	Acc#
	sp:YVBG_BACSU	032244

Description

HYPOTHETICAL 22.6 KD PROTEIN IN OPUCA-ENO INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
895290_c2_83	4542	9764	189	570	137	7.6e-08

Protein name	Locus Name	Acc#
	sp:YN23_YEAST	P53832

Description

PRECURSOR

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
9.09513_c2_78.....	4543	9765	253	762		

Protein name	Locus Name	Acc#
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10578415_t2_20.....	4544	9766	1360	4083	335	2.0e-41

Protein name	Locus Name	Acc#
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adenylate cyclase homolog	pir:T17197	T17197
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10737900_E3_43	4545	9767	221	666	140	9.3e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
AnSH phosphatase	gp:SCAHBAGC2	AF131879

Description

Streptomyces collinus ansatrienin AHBA biosynthetic gene clusterregion 2, complete sequence.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_E2_28	4546	9768	159	477	535	1.8e-51

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:JQ1020	JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_E3_32	4547	9769	431	1296	1723	2.3e-177

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:JQ1020	JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19537503_E1_8	4548	9770	188	567		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
1960876_f1_2	4549	9771	500	1503	96	0.0095		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
putative glucosyl hydrolase precursor				gp:AF047839	AF047839			
<u>Description</u>								
Pseudoalteromonas sp. S9 putative glucosyl hydrolase precursor and adaptive response regulatory protein (ada) genes, complete cds.								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
19688778_c3_87	4550	9772	301	906	165	6.6e-12		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
MsmR				gp:SPU49397	U49397			
<u>Description</u>								
Streptococcus pyogenes MsmR (msmR) gene, partial cds; LepA (lepA), Cpa (cpa), and Nra (nra) genes, complete cds; SsbA (ssbA) gene, partial cds; and unknown genes.								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
20704052_c3_82.....	4551	9773	465	1398	380	4.7e-35		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
hypothetical protein PAB0790				pir:H75098	H75098			
<u>Description</u>								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
22860128_f1_3.....	4552	9774	83	252	64	0.031		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
				sp:SPRC_XENLA	P36378			
<u>Description</u>								
(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)								

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_f3_49	4553	9775	83	252	64	0.031

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:SPRC_XENLA	P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24229677_c2_64	4554	9776	225	678		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2507010_f2_13.....	4555	9777	349	1050	213	4.2e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PH1107	pir:D71051	D71051

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25798155_f3_36.....	4556	9778	71	216		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33442_f1_9	4557	9779	390	1173	153	1.5e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transcription regulator AraC/XyIS family homolog ydeE	pir:G69777	G69777

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33625407_c1_50.....	4558	9780	118	357	119	1.6e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transposase	gp:AF038866	AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) andmobilization protein BmpH (bmpH) genes, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35555187_c3_80.....	4559	9781	112	339	111	1.2e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transposase	gp:AF038866	AF038866

Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) andmobilization protein BmpH (bmpH) genes, complete cds.
--

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36361510_f1_10.....	4560	9782	157	474	116	4.5e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein MTH628	pir:E69183	E69183

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36523937_c2_72	4561	9783	658	1977	243	4.7e-34

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sialic acid-specific 9-O-acetylesterase	gp:MMAS90A	X98625

Description

M.musculus mRNA for sialic acid-specific 9-O-acetylesterase.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4095062_c1_53	4562	9784	514	1545	90	0.00020

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
oligopeptide ABC transporter, ATP-binding protein	pir:D72289	D72289

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4103816_c1_57	4563	9785	70	213		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4110010_f3_47	4564	9786	82	249		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4884682_c2_65	4565	9787	74	225		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
548762_f2_21	4566	9788	220	663	429	3.0e-40

Protein name Locus Name Acc#

sp:YJV8_YEAST P40892

Description

(EC 2.3.1.-)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
587763_f3_41	4567	9789	170	513	212	3.0e-17

Protein name Locus Name Acc#

hypothetical protein TM0383 pir:G72383 G72383

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6364505_f3_29	4568	9790	260	783		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7031556_f1_11	4569	9791	174	525		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
8.6.6.5.3.7_f3_3.5.....	4570	9792	654	1965	354	4.4e-40

Protein name Locus Name Acc#

alpha-glucosidase	gp:BTU66897	U66897
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Description

Bacteroides thetaiotaomicron neopullulanase (susA) and alpha-glucosidase (susB) genes, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15.0.9.7.18.7_f3_3.8.....	4571	9793	118	357		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
17.0.7.4.0.6.3_f2_13.....	4572	9794	98	297		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
193757_E2_27	4573	9795	788	2367	830	9.8e-83

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20820162_E2_11.....	4574	9796	597	1794	1587	5.9e-163

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive 87KD antigen PG92	gp:AF175724	AF175724

Description

Porphyromonas gingivalis strain W50 immunoreactive 87KD antigen PG92 gene, complete cds.
--

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22478383_E3_37.....	4575	9797	188	567	215	1.4e-17

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
RNA polymerase ECF-type sigma factor sigW	pir:H69706	H69706

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22698312_E1_7.....	4576	9798	359	1080		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24023387_f2_12	4577	9799	839	2520	1103	1.2e-111

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative secreted beta-galactosidase	gp:SCF81	AL133171

Description

Streptomyces coelicolor cosmid F81.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24219562_f1_9	4578	9800	292	879	338	1.3e-30

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:S76053	S76053

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25484661_f2_20.....	4579	9801	567	1704	1736	9.6e-179

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ABC transporter (ATP-binding protein) homolog ykpA	pir:E69861	E69861

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25595943_f2_10.....	4580	9802	68	207		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
NO-HIT		

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26306512_c1_56	4581	9803	395	1188	1301	1.2e-132

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive heat shock protein DnaJ	gp:AF145797	AF145797

Description

Porphyromonas gingivalis strain W50 immunoreactive heat shock protein DnaJ gene, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34181503_f1_2	4582	9804	544	1635	130	5.1e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
outer membrane protein	gp:BNROMPBP	L77614

Description

Bacteroides thetaiotaomicron outer membrane protein (susD) gene, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34553375_c2_78.....	4583	9805	83	252		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35797208_f2_14.....	4584	9806	841	2526	407	1.1e-70

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36360255_F2_26	4585	9807	347	1044	261	1.9e-22

Protein name Locus Name Acc#
sp:PLC_BACCE P14262

Description

(PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36540925_F2_25	4586	9808	85	258		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4328182_C3_8.9.....	4587	9809	353	1062	149	5.7e-07

Protein name Locus Name Acc#

surface antigen BspA pir:T31094 T31094

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4879627_F1_8.....	4588	9810	292	879	259	3.1e-22

Protein name Locus Name Acc#

probable transmembrane protein pir:T34651 T34651

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
6283150_f1_1	4589	9811	261	786	789	2.2e-78		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>		
immunoreactive 87KD antigen PG92				gp:AF175724		AF175724		
<u>Description</u>								
Porphyromonas gingivalis strain W50 immunoreactive 87KD antigenPG92 gene, complete cds.								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
6640682_c1_55	4590	9812	255	768	309	1.6e-27		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>		
				sp:GREP_FRATU		P48204		
<u>Description</u>								
GRPE PROTEIN								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
10.000.026.1_c3_25.0	4591	9813	297	894	603	1.1e-58		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>		
integrase				gp:BFU75371		U75371		
<u>Description</u>								
Bacteroides fragilis transposon Tn4555 TnpA (tnpA), integrase(int), TnpC (tnpC), excisionase (xis), mobilization protein (mobA), and beta-lactamase (cfxA) genes, complete cds; and unknown genes.								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
10.5.5.15.3_c3_25.5	4592	9814	573	1722	373	5.3e-34		
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>		
hypothetical protein s110855				pir:S74833		S74833		
<u>Description</u>								

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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1203515_c3_268	4593	9815	60	183		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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13.75.0040_c1_15.9.....	4594	9816	80	243		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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13.75.950.7_f3_114.....	4595	9817	304	915	159	5.9e-10
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein jhp0651	pir:E71905	E71905
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<u>Description</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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13.78.2212_f3_105.....	4596	9818	82	249		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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13.88.2712_f2_84.....	4597	9819	87	264		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14970628_c1_165	4598	9820	547	1644	355	1.3e-53

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
K+ transport protein homolog	pir:H70430	H70430

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16.054635_E2_70	4599	9821	208	627		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16433140_E3_253	4600	9822	76	231		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
166.95462_E3_104	4601	9823	68	207		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16.832885_c1_166	4602	9824	431	1296	1723	2.3e-177

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein	pir:JQ1020	JQ1020
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
176875_c1_156	4603	9825	194	585		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
189010_f1_28	4604	9826	1198	3597	111	1.5e-06

Protein name Locus Name Acc#

sp:YY02_METJA Q60301

Description

HYPOTHETICAL PROTEIN MJECS02

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19726387_f1_8	4605	9827	490	1473	2625	6.0e-273

Protein name Locus Name Acc#

sp:CATB_BACFR P45737

Description

CATALASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19959762_c2_184	4606	9828	1167	3504		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20101577_f1_50	4607	9829	334	1005	514	3.0e-49

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hemin permease	pir:S54438	S54438

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20110930_f1_14	4608	9830	461	1386	1259	3.4e-128

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
tryptophan synthase, subunit beta (trpB-1) homolog	pir:G69404	G69404

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20312527_c3_266	4609	9831	203	612	203	2.7e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
RNA polymerase sigma factor SigZ-like protein	gp:AF137263	AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20320177_f2_75	4610	9832	278	837	103	0.0042

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
branched-chain amino acid ABC transporter, ATP-binding protein (braG-4) homolog	pir:D69423	D69423

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20422203_f3_101	4611	9833	305	918	941	1.7e-94

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:END4_ECOLI	

Description

ENDONUCLEASE IV, (ENDODEOXYRIBONUCLEASE IV)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20517142_f2_74	4612	9834	855	2568		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2.07.06.6.7.8_c2_1.7.7	4613	9835	83	252		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2.11.5.6.2.5_c2_2.0.7	4614	9836	285	858	107	1.1e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:YZ35_METJA	Q60291
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Description

HYPOTHETICAL PROTEIN MJECL35

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2150262_f1_22	4615	9837	194	585		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2173.9427_f1_21	4616	9838	161	486		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
223.86.0.0.7_c1_16.0	4617	9839	65	198		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2246.17.13_f2_6.9	4618	9840	82	249	101	3.9e-05

Protein name Locus Name Acc#

gp:BP053767 U53767

Description

Bacillus pumilus plasmid pSH1452, Rep gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_c2_211	4619	9841	83	252	64	0.031

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:SPRC_XENLA	P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23478176_f1_25	4620	9842	124	375	94	0.00045

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
TnpC	gp:BFU75371	U75371

Description

Bacteroides fragilis transposon Tn4555 TnpA (tnpA), integrase(int), TnpC (tnpC), excisionase (xis), mobilization protein (mobA), and beta-lactamase (cfxA) genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23628262_f2_86.....	4621	9843	70	213	53	0.0033

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein BB0404	pir:C70150	C70150

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23992136_f1_7.....	4622	9844	849	2550	323	4.9e-39

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative alpha-glucosidase	gp: AAC252161	AJ252161

Description

Alicyclobacillus acidocaldarius maltose/maltodextrine transport gene region (maleFGR genes, cdaA gene and glcA gene).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24020312_c2_221	4623	9845	962	2889	436	2.7e-37

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2423.7.76.2_c1_1.76.....	4624	9846	325	978		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
242413.7.7_c3_9.3.....	4625	9847	320	963	1564	1.6e-160

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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beta-lactamase, A precursor:cephalosporinase	pir:140192
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24329.7.02_c2_18.2.....	4626	9848	174	525	79	0.036

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF048749	AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24415932_f3_107	4627	9849	422	1269	119	0.00030

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:Y665_HAEIN	P44033

Description

HYPOTHETICAL PROTEIN HI0665

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648550_f3_109	4628	9850	213	642		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25658441_c2_222.....	4629	9851	69	210		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25945152_f2_71.....	4630	9852	1215	3648	93	0.014

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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rhoptry protein	pir:T28676	T28676
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26594683_c2_185	4631	9853	728	2187		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26597832_f3_113.....	4632	9854	679	2040		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.0.06.3.7.7_f2_66.....	4633	9855	98	297	113	4.0e-06

Protein name Locus Name Acc#

AbiEii gp:LLU36837 U36837

Description

Lactococcus lactis plasmid pNP40, abortive infection locus, AbiEi,AbiEii, RecA(LP), AbiF genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.0128208_c2_206.....	4634	9856	96	291		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32243757_f1_26	4635	9857	89	270		

Protein name _____ Locus Name _____

Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34257.7.52_c2_216.....	4636	9858	369	1110	209	7.6e-24

Protein name _____

Locus Name _____

Acc# _____

sp:XYLB_BACOV P49943

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
345.7.8410_c3_254.....	4637	9859	72	219		

Protein name _____

Locus Name _____

Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.56.6.5952_f3_95.....	4638	9860	127	384	644	5.0e-63

Protein name _____

Locus Name _____

Acc# _____

hypothetical protein 2 pir:I40233 I40233

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.5.7.9296.7_c2_183.....	4639	9861	660	1983	2579	4.5e-268

Protein name _____

Locus Name _____

Acc# _____

DnaK	gp:AB015879	AB015879
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Description

Porphyromonas gingivalis dnaK operon genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3959627_c3_225	4640	9862	196	591	295	4.8e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ORF5	gp:AB015879	AB015879

Description

Porphyromonas gingivalis dnaK operon genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4147126_f1_32	4641	9863	318	957	534	2.3e-51

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
5'-nucleotidase	gp:CL1131243	AJ131243

Description

Columba livia mRNA for 5'-nucleotidase.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
417353.0_c2_192.....	4642	9864	62	189		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

<u>NO-HIT</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
42700_c1_167.....	4643	9865	95	288	163	3.1e-11

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Na ⁺ -ATPase chain J:protein slr1509:protein slr1509	pir:S75455	S75455
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4727280_f2_87	4644	9866	396	1191	277	8.9e-23

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:Y878_METJA	Q58288

Description

HYPOTHETICAL PROTEIN MJ0878

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4727337_f1_29	4645	9867	536	1611	127	1.4e-13

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PAB1002	pir:G75064	G75064

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4954832_f2_55.....	4646	9868	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5274003.cl_138.....	4647	9869	724	2175	438	3.0e-52

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
otnA protein	pir:S70958	S70958

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
9798467.cl_140.....	4648	9870	78	237		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
984805_c1_168	4649	9871	233	702	294	6.2e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein aq_1503	pir:G70430	G70430

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1211062_f2_93	4650	9872	84	255	90	0.0068

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
Cry1A toxin receptor A	gp:AF173552	AF173552

Description

Heliothis virescens Cry1A toxin receptor A mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1226510_c1_222	4651	9873	448	1347	319	1.3e-31

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative putrescine/spermidine binding protein	gp:PSEPAHP	L49465

Description

Pseudomonas fluorescens hypothetical metabolite transport protein, positive transcriptional regulator (phnR), phosphonoacetatehydrolase (phnA), 2-phosphonopropionate transporter (phnB), putative putrescine/spermidine binding protein, and putativemethionine sulfoxide reductase genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13906285_f1_29	4652	9874	1069	3210	393	1.8e-48

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
histidine protein kinase homolog Gacs	gp:AF197912	AF197912

Description

Azotobacter vinelandii histidine protein kinase homolog Gacs (gacS) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14225953_f3_194	4653	9875	65	198	158	1.6e-11

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein APE2061	pir:G72510	G72510

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14485880_f1_53	4654	9876	395	1188	206	4.5e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:TLPA_BRAJA	P43221

Description

PROTEIN TLPA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14539662_f3_160	4655	9877	204	615	308	2.0e-27

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein MTH671	pir:D69189	D69189

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14630035_c2_271	4656	9878	597	1794	1319	1.5e-134

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable V-type ATPase, subunit A (atpA-1)	pir:G71325	G71325

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15712666_f1_24	4657	9879	198	597	222	2.6e-18
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
				sp:YJJP_HAEIN	P44520	

Description

HYPOTHETICAL PROTEIN HI0108

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15719042_c2_270	4658	9880	296	891	93	5.1e-06
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
hypothetical protein BB0095				pir:G70111	G70111	

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1653.9.03.8...c3...351.....	4659	9881	199	600	427	5.0e-40
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
2-keto-3-deoxygluconate kinase				pir:G72422	G72422	

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16610827_f1_3.7.....	4660	9882	468	1407	753	1.4e-74
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
Na ⁺ /H ⁺ antiporter (nhaC-1) homolog				pir:D70179	D70179	

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16833455_c2_316	4661	9883	304	915	589	3.4e-57

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
cation efflux system protein	gp:AF203881	AF203881

Description

Zymomonas mobilis strain ZM4 clone 43F4, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19687750_c1_228	4662	9884	75	228		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2.09.72.755..13..146.....	4663	9885	85	258	78	0.0019

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:PRS6_MANSE	P46507

Description

26S PROTEASE REGULATORY SUBUNIT 6B (ATPASE MS73)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21515678_c3_334.....	4664	9886	865	2598	1621	1.5e-166

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PH1512	pir:D71027	D71027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22445301_f2_87	4665	9887	231	696	122	2.0e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF125164	AF125164

Description

Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22454707_f3_161	4666	9888	356	1071	1394	1.7e-142

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:RIR2_TREPA	083092

Description

(RIBONUCLEOTIDE REDUCTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23595180_c1_266	4667	9889	403	1212	268	1.7e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YRKO_BACSU	P54442

Description

HYPOTHETICAL 46.4 KD PROTEIN IN BLTR-SPOIIIC INTERGENIC REGION
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23631627_c1_213	4668	9890	444	1335	1018	1.2e-102

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable V-type ATPase, subunit B (atpB-1)	pir:H71325	H71325

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24253311_f3_167	4669	9891	405	1218	213	3.9e-15

Protein name Locus Name Acc#

gp:AB016260

Description

Agrobacterium tumefaciens plasmid pTi-SAKURA, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24257692_f1_9	4670	9892	599	1800	649	1.5e-63

Protein name Locus Name Acc#

TonB-dependent receptor HmuR gp:PGU87395 U87395

Description

Porphyromonas gingivalis TonB-dependent receptor HmuR (hmuR) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24347153_c3_33.0	4671	9893	623	1872	559	5.1e-54

Protein name Locus Name Acc#

V-type ATPase, subunit I homolog pir:C70111 C70111

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24509627_c3_35.0	4672	9894	142	429	494	3.9e-47

Protein name Locus Name Acc#

2-keto-3-deoxygluconate kinase pir:G72422 G72422

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24806567_c1_238	4673	9895	119	360	245	9.6e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein MTH1285	pir:A69038	A69038

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25469832_t3_184	4674	9896	252	759	824	4.2e-82

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
30S ribosomal protein S16-like protein	gp:AF137263	AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25984388_t1_47	4675	9897	447	1344		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26288442_c3_348	4676	9898	154	465	233	1.8e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein yvbK	pir:B70030	B70030

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26365691_c2_287	4677	9899	243	732	184	1.0e-22

Protein name Locus Name Acc#

hypothetical protein pir:B75629 B75629

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29337830_c1_231	4678	9900	371	1116	214	7.6e-25

Protein name Locus Name Acc#

hypothetical protein pir:H75628 H75628

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29589842_c2_268	4679	9901	65	198		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30493775_c3_332	4680	9902	61	186		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31461016_c3_380	4681	9903	515	1548	700	5.8e-69

Protein name Locus Name Acc#

sp:YHCA_BACSU P54585

Description

HYPOTHETICAL 58.3 KD PROTEIN IN GLPD-CSPB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31833126_f2_86	4682	9904	309	930	106	0.021

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable erythrocyte-binding protein MAEBL	pir:T09129	T09129

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32042553_c2_317	4683	9905	61	186		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32234752_f2_91	4684	9906	117	354	73	0.016

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein MTH670	pir:C69189	C69189

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.3236.050_c3_3.77	4685	9907	138	417		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.3401552_c1_230	4686	9908	211	636	386	1.1e-35

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
peptide chain release factor homolog prfH	pir:E64748	E64748

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33711081_f2_136	4687	9909	99	300	111	2.4e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	gp:SSU18930	Y18930

Description

Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3398466_f2_90	4688	9910	1467	4404	687	4.4e-125

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
cobalamin biosynthesis protein N	pir:C69048	C69048

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34065926_c1_265.....	4689	9911	231	696	231	5.8e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein aq_1060	pir:D70391	D70391

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34081405_c1_212.....	4690	9912	88	267	110	1.9e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PHS004	pir:F71245	F71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34242285_c1_221	4691	9913	269	810	469	1.8e-44
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
spermidine/putrescine ABC transporter, permease protein (potC) homolog				pir:G70179		G70179

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34648557_c2_279	4692	9914	137	414		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35352135_c3_33.9	4693	9915	417	1254	97	0.038

Protein name

Locus Name

Acc#

hypothetical protein DKFZp566D1824.1

pir:T14767

T14767

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3926531_f2_94	4694	9916	260	783	257	5.1e-22

Protein name

Locus Name

Acc#

sp:YJJP_ECOLI

P39402

Description

HYPOTHETICAL 30.5 KD PROTEIN IN DNAT-BGLJ INTERGENIC REGION (F277)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
3939211_f2_89	4695	9917	185	558	206	1.4e-15		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
TonB-dependent receptor HmuR				gp:PGU87395	U87395			
<u>Description</u>								
Porphyromonas gingivalis TonB-dependent receptor HmuR (hmuR) gene, complete cds.								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
4069152_c1_241	4696	9918	227	684	262	1.5e-22		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase				pir:F72422	F72422			
<u>Description</u>								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
4103530_c3_326.....	4697	9919	199	600	152	6.9e-11		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
V-type ATPase, subunit E homolog				pir:H70111	H70111			
<u>Description</u>								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
4148892_c1_217.....	4698	9920	220	663				
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
<u>Description</u>								
NO-HIT								

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
489680_f1_43	4699	9921	130	393		

Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
49.0027.6_f2_92	4700	9922	840	2523	2812	9.2e-293

Protein name

Locus Name

Acc#

sp:RIR1_TREPA

083972

Description

(RIBONUCLEOTIDE REDUCTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
49.56.5.3.7_f1_17	4701	9923	234	705	99	0.012

Protein name

Locus Name

Acc#

conserved hypothetical protein AF1223

pir:F69402

F69402

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
49.6.0.9.6.7_f3_145	4702	9924	79	240		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
501952_c3_336	4703	9925	470	1413	1004	3.6e-101

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
spermidine/putrescine ABC transporter, ATP-binding protein (potA) homolog	pir:A70180	A70180

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.285.927_c1_214.....	4704	9926	204	615	231	2.9e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable V-type ATPase, subunit D (atpD-1)	pir:A71326	A71326

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.892183_c3_342.....	4705	9927	439	1320	1009	1.1e-101

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
rtcB protein	pir:D75521	D75521

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.9.0.9512_c3_3.33.....	4706	9928	593	1782	427	4.8e-60

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
UDPglucose--glycogen glucosyltransferase,, skeletal muscle:glycogen(starch) synthase:glycogen(starch) synthase	pir:A33369	

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6912588_c2_278	4707	9929	268	807	426	6.3e-40

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
spermidine/putrescine ABC transporter, permease protein (potB) homolog	pir:H70179	H70179

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7.072953_c1_243	4708	9930	72	219		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7.81561_c3_338	4709	9931	133	402	294	6.2e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glycine-rich RNA-binding protein (clone A81)	pir:S31443	S31443

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7.9153.7_c1_225	4710	9932	688	2067	55	0.036

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:CPU53466	U53466

Description

Cydia pomonella granulosis virus ORF13L gene, partial cds, ORF15L, ORF15R, ORF16L, ORF17L genes, complete cds, ORF17R gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
970262_c2_274	4711	9933	163	492	228	6.1e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PH1980	pir:D71214	D71214

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
975186_c3_379	4712	9934	540	1623	749	3.7e-74

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YIDE_HAEIN	P44472

Description

HYPOTHETICAL PROTEIN HI0035

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11882928_f1_24	4713	9935	65	198		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11929010_f1_30	4714	9936	75	228		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1192950_f1_6	4715	9937	67	204		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1211125.02_c3_184	4716	9938	519	1560		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1253.56.8.7_f2_39	4717	9939	735	2208	580	3.4e-76

Protein name Locus Name Acc#

hypothetical protein TM0280	pir:F72395	F72395
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12828.07_c2_129	4718	9940	64	195	53	0.017

Protein name Locus Name Acc#

sp:RYL2_YARLI	P41925
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Description

RAS-LIKE GTP-BINDING PROTEIN RYL2

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13066438_f2_54	4719	9941	88	267		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13.7.9855.2_f2_57	4720	9942	69	210		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14.7.09.7.01_c1_123	4721	9943	363	1092	521	5.4e-50

Protein name Locus Name Acc#

FucR gp:AF137263 AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
18.7.6.3.7_c2_13.0	4722	9944	641	1926		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22353385_f2_44	4723	9945	157	474	313	6.0e-28

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein slr0698	pir:S77038	S77038

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22939206_c1_101	4724	9946	393	1182	908	5.3e-91

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:H72299	H72299

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23615930_c3_176	4725	9947	696	2091	457	3.1e-41

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:BGAL_THETU	P26257

Description

BETA-GALACTOSIDASE, (LACTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23625926_c1_126	4726	9948	390	1173	246	6.8e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF141932	AF141932

Description

Rhizobium leguminosarum bv. trifolii plasmid PRle162Y10C rspDEF operon, partial sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24259438_c1_125	4727	9949	204	615	98	0.026

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
protein kinase,, cGMP-dependent	pir:B28269	B28269

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
243353.01..t2..43.....	4728	9950	606	1821	1237	7.3e-126

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:LCFH_HAEIN	P44446

Description

ACYL-COA SYNTHETASE) (LACS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
246268.76..f3..6.3.....	4729	9951	469	1410		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
246407.62..c1..9.5.....	4730	9952	380	1143		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
265950.67..f1..15.....	4731	9953	433	1302	244	3.7e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein MTH1451	pir:C69060	C69060
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29462801_f1_2	4732	9954	62	189		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.3.7.2.96.7.5_f3_6.5	4733	9955	848	2547	313	8.0e-26

Protein name Locus Name Acc#

putative alpha-L-arabinofuranosidase gp:ATAC011708 AC011708

Description

Arabidopsis thaliana chromosome III BAC T7M13 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.417.8.3.05_f1_14	4734	9956	444	1335	146	5.3e-07

Protein name Locus Name Acc#

sp:PORP_PSEAE P05695

Description

PORIN P PRECURSOR (OUTER MEMBRANE PROTEIN D1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.425.2.17.6_c1_9.3	4735	9957	84	255	116	1.1e-05

Protein name Locus Name Acc#

Styrene sensor kinase gp:PSSTYCATA AJ000330

Description

Pseudomonas sp. DNA for styrene catabolism genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34406517_c2_127	4736	9958	1119	3360	826	7.2e-97

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (RagA)	gp:PGI130872	AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34410751_f3_75	4737	9959	860	2583	419	3.1e-37

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF007381	AF007381

Description

Flavobacterium johnsoniae gliding motility protein (glmA) gene, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.9.0.7.25.3_f3_66.....	4738	9960	882	2649	1066	1.1e-127

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein SCF34.07	pir:T36406	T36406

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4.1.7.6.4.6.2_c2_128.....	4739	9961	272	819		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

<u>NO-HIT</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
424193_f3_71	4740	9962	354	1065	697	1.2e-68

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:RF2_ECOLI

Description

PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4330312_c1_98	4741	9963	306	921	160	8.0e-13

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein	pir:T33724	T33724
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4689392_f1_1.....	4742	9964	135	408		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5345192_c1_99.....	4743	9965	514	1545	705	1.7e-69

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:HEXA_PORGI	P49008
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Description

(BETA-NAHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
587787_c2_131	4744	9966	404	1215	400	3.6e-37

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unsaturated glucuronyl hydrolase	gp:AB019619	AB019619

Description

Bacillus sp. GLI genes for orf and unsaturated glucuronylhydrolase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
593950_c1_94	4745	9967	474	1425	451	2.6e-42

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
adenylate cyclase	gp:D89625	D89625

Description

Anabaena sp. cyaC gene for adenylate cyclase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.81283.7...c3...186.....	4746	9968	370	1113	269	2.7e-23

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable succinyl-diaminopimelate desuccinylase	pir:H70608	H70608

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1.096.9.7.03...f2...10.....	4747	9969	170	513		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13765751_f2_15	4748	9970	299	897	143	3.3e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
cytochrome b	gp:GPA249395	AJ249395

Description

Globodera pallida mitochondrial COII, ND4, COIII, ND6, ND1, ND3 and cyt b genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13838463_f2_11	4749	9971	69	210		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15.7.0.9.7.8.8...f3...17.....	4750	9972	405	1218		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
216.4.6.9.15...f2...8.....	4751	9973	246	741		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22848775_c1_23	4752	9974	199	600	92	0.00035

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:DNU4_RHORU	P15017

Description

PROBABLE TRANSCRIPTIONAL REGULATOR IN ATPASE CF(0) REGION (URF4)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23444088_c1_24	4753	9975	85	258		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25834567_f1_1	4754	9976	244	735	75	0.039

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp: MUSIGKBJ	M13606

Description

Mouse Ig active kappa-chain VJ2 mRNA from HP22.134.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29859506_f2_7	4755	9977	183	552		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
34570927_f1_2	4756	9978	329	990		

Protein name Locus Name Acc#

Description

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
36142837_c3_40	4757	9979	65	198	78	0.021

Protein name Locus Name Acc#

hypothetical protein C17F3.3 pir:T32879 T32879

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4162818_f2_14	4758	9980	133	402	72	0.021

Protein name Locus Name Acc#

conserved hypothetical protein BBI40 pir:G70244 G70244

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
5859640_f2_9	4759	9981	422	1269	88	0.0055

Protein name Locus Name Acc#

unknown gp:AF033858 AF033858

Description

Pediococcus pentosaceus strain ATCC43200 plasmid pMD136, complete plasmid sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11769375_c2_42	4760	9982	681	2046	240	4.1e-25

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (RagA)	gp:PGI130872	AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16579388_c3_46	4761	9983	190	573	401	2.8e-37

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:Y4PL_RHISN	P55617

Description

PUTATIVE INSERTION SEQUENCE ATP-BINDING PROTEIN Y4PL

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20265_c1_37.....	4762	9984	89	267		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32501380_E3_28.....	4763	9985	130	393		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34181512_c2_38	4764	9986	207	624		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
364297763_c1_34	4765	9987	79	240	66	0.011

Protein name Locus Name Acc#

gp:ATAC011020 AC011020

Description

Arabidopsis thaliana chromosome 1 BAC F12B7 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4098562_f1_4	4766	9988	92	279	77	0.015

Protein name Locus Name Acc#

probable sigK protein pir:F70830 F70830

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5275442_c3_47	4767	9989	156	471		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
85151_c2_41	4768	9990	299	900	436	7.4e-40
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein					pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14885458_c2_3	4769	9991	600	1803	563	1.9e-54
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
					sp:BGAL_THETU	P26257

Description

BETA-GALACTOSIDASE, (LACTASE)						
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10837887_c3_30	4770	9992	374	1125	1011	6.5e-102
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
CDP-glucose-4,6-dehydratase					pir:D47070	D47070

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14640675_c3_31	4771	9993	298	894	950	1.9e-95
<u>Protein name</u>					<u>Locus Name</u>	<u>Acc#</u>
CDP-tyvelose epimerase					gp:YPU29691	U29691

Description

Yersinia pseudotuberculosis group
IVACDP-4-keto-6-deoxy-D-glucose-3-dehydrase (ddhC) gene, partial
cds, CDP-paratose synthetase (prt) and CDP-tyvelose epimerase (tyv) genes, complete cds, and putative O antigen export protein (wzx) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
20312800_c1_22	4772	9994	306	921	225	1.3e-18		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
dTDP-glucose 4,6-dehydratase				pir:H69105	H69105			
<u>Description</u>								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
20507213_c3_29	4773	9995	86	261				
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
<u>Description</u>								
NO-HIT								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
24880278_t2_12	4774	9996	81	246				
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
<u>Description</u>								
NO-HIT								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
391531_t1_5	4775	9997	69	210				
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
<u>Description</u>								
NO-HIT								
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>		
46378150_c1_20	4776	9998	285	858	475	4.1e-45		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>			
glucose-1-phosphate cytidylyltransferase,				pir:C47070	C47070			
<u>Description</u>								

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13070915_c1_11	4777	9999	845	2538	679	3.4e-66

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4400952_c3_13.....	4778	10000	264	795	445	8.0e-41

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10635936_f1_15.....	4779	10001	419	1260		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11829203_c1_283.....	4780	10002	270	813	132	2.5e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:D86934	D86934

Description

Staphylococcus aureus genes, mec region, partial and complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12298437_c2_380	4781	10003	321	966	252	1.7e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YYAM_BACSU	P37511

Description

HYPOTHETICAL 32.9 KD PROTEIN IN TETB-EXOA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13865675_c1_304	4782	10004	312	939	964	6.2e-97

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
homoserine O-succinyltransferase	pir:C72324	C72324

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13868955_c3_200.....	4783	10005	111	336		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1407956_c3_406.....	4784	10006	147	444		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14640762_f2_103	4785	10007	86	261		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
146577000_c1_3.01	4786	10008	642	1929	155	2.3e-10

Protein name Locus Name Acc#
conserved hypothetical protein pir:E75439 E75439

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15703215_f3_26.6	4787	10009	61	186		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
159562_f1_41	4788	10010	74	225	209	6.3e-17

Protein name Locus Name Acc#
sp:FER_BUTME P14073

Description

FERREDOXIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16615912_f3_261	4789	10011	67	204		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16832885_c2_358.....	4790	10012	431	1296	1723	2.3e-177

Protein name Locus Name Acc#
hypothetical protein pir:JQ1020 JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19689075_c1_334.....	4791	10013	867	2604	453	1.5e-39

Protein name Locus Name Acc#
hypothetical protein F10M10.30 pir:T04772 T04772

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19710881_f1_89.....	4792	10014	216	651	79	0.012

Protein name Locus Name Acc#
gp:TCU64729 U64729

Description

Toxocara canis Tch SLdT.460 mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19770066_c2_351	4793	10015	389	1170	652	7.1e-64

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
potassium-dependent ATPase subunit D'	gp:AF213466	AF213466

<u>Description</u>
Anabaena sp. L-31 kdp operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20119033_f1_10	4794	10016	191	576	144	4.1e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:PNUC_SALTY	P24520

Description

PNUC PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2.0.4.6.8.7_c2_352.....	4795	10017	64	195		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22298176_f1_91.....	4796	10018	62	189		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22306532_f2_123	4797	10019	530	1593	836	6.0e-87

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:S76076	S76076

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860128_c3_415.....	4798	10020	83	252	64	0.031

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:SPRC_XENLA	P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22860636_c3_431.....	4799	10021	415	1248	862	4.0e-86

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable phosphonopyruvate decarboxylase, 1	pir:D69154	D69154

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23626711_c3_404.....	4800	10022	687	2064	2134	6.4e-221

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
potassium-transporting ATPase, B subunit	pir:A75627	A75627

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23632875_c3_403	4801	10023	573	1722	1228	6.5e-125

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
potassium-translocating ATPase A chain	gp: AAC243194	AJ243194

Description

Alicyclobacillus acidocaldarius kdpA gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23960013_c3_418	4802	10024	954	2865	935	2.4e-115

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative secreted protein	gp: SCF41	AL117387

Description

Streptomyces coelicolor cosmid F41.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24007761_c1_297	4803	10025	986	2961		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24322063_c2_362	4804	10026	333	1002		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24322712_c1_295	4805	10027	1152	3459	754	5.3e-132

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24334692_f3_240	4806	10028	222	669		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24640915_f2_106	4807	10029	209	630	297	3.0e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein Jhp1211	pir:C71832	C71832

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24642818_f2_187	4808	10030	118	357	98	3.6e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:SSK3MECA1	Y13052

Description

S.sciuri mecA1 gene, strain K3 (MM2).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24804691_c1_298	4809	10031	257	774		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24820326_c1_322.....	4810	10032	290	873	607	1.2e-58

Protein name Locus Name Acc#

aspartate kinase, / homoserine dehydrogenase,
T16H5.70:protein T16H5.70:protein T16H5.70

pir:T04752

T04752

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24866706_c1_293.....	4811	10033	447	1344	423	1.5e-39

Protein name Locus Name Acc#

VicK protein gp:EFA012050 AJ012050

Description

Enterococcus faecalis vic operon and flanking genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25277_c3_411.....	4812	10034	798	2397		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2557712_c1_333	4813	10035	208	627	167	1.8e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein s110687	pir:S74416	S74416

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25835942_c2_385	4814	10036	336	1011	131	7.6e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:FECR_ECOLI	P23485

Description

FECR PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25945887_c3_417	4815	10037	401	1206	983	6.0e-99

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:AAT_BACST	Q59228

Description

ASPARTATE AMINOTRANSFERASE, (TRANSAMINASE A) (ASPAT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29720927_c1_321	4816	10038	527	1584	788	2.8e-78

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:AK_METJA	Q57991

Description

PROBABLE ASPARTOKINASE, (ASPARTATE KINASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3001402_f3_222	4817	10039	212	639	115	1.9e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:SCU40158	U40158

Description

Staphylococcus carnosus response regulator-like protein (orfx) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30656255_c1_294	4818	10040	193	582	316	2.9e-28

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
RNA polymerase sigma factor SigZ-like protein	gp:AF137263	AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30661682_f2_185.....	4819	10041	486	1461	379	8.2e-35

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative aspartate kinase	gp:ATAC010797	AC010797

Description

Arabidopsis thaliana chromosome III BAC F28J7 genomic sequence, complete sequence.
--

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30720407_c2_349.....	4820	10042	234	705	359	8.0e-33

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ATKC_MYCTU	P96369

Description

C CHAIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3125011_f3_223	4821	10043	811	2436	253	1.1e-29

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
SfTP	gp:AF126201	AF126201

Description

Pseudomonas putida strain S-313 sulfate ester desulfurization gene locus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3132040_f2_120	4822	10044	385	1158	728	6.3e-72

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ASG1_ECOLI	P18840

Description

(L-ASNASE 1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32188_f2_186.....	4823	10045	836	2511	971	1.1e-97

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
NADH oxidase (noxA-3) homolog	pir:H69299	H69299

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.34.8.6.5.0.2...c3_408.....	4824	10046	340	1023	114	0.00068

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transmembrane sensor	gp:AF051691	AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor (fiuI), transmembrane sensor (fiuR), and hydroxamate-type ferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35245635_c3_410	4825	10047	511	1536	129	2.4e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:U96771	U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36375662_c1_323	4826	10048	451	1356	939	2.8e-94

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:THRC_HAEIN	P44503

Description

THREONINE SYNTHASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3912663_f2_122.....	4827	10049	462	1389	1242	2.1e-126

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:RADA_BACSU	P37572

Description

DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS HOMOLOG)
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3939387_c3_437.....	4828	10050	305	918	551	3.6e-53

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative 30.6 kDa protein	gp:AF037440	AF037440

Description

Edwardsiella ictaluri D-3-phosphoglycerate dehydrogenase (serA) gene, partial cds; ribose-5-phosphate isomerase (rpiA), inhibitor of chromosome initiation (ic1A), putative 26 kDa protein (yggE), putative 30.6 kDa protein (yggB), and fructose 1,6-bisphosphate aldolase (fda) genes, complete cds; and phosphoglycerate kinase (pgk) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3942202_c2_339	4829	10051	489	1470	267	2.9e-38

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ARSF_HUMAN	P54793

Description

ARYLSULFATASE F PRECURSOR, (ASF)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4078255_c1_281	4830	10052	494	1485	496	2.4e-47

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
tripeptidyl aminopeptidase	gp:STMTPAP	L46588

Description

Streptomyces lividans tripeptidyl aminopeptidase gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4103410_c3_390.....	4831	10053	657	1974		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4414086_c1_289.....	4832	10054	467	1404	859	8.3e-86

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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response regulatory protein (rrp-2) homolog	pir:B70195	B70195
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4694087_c2_359	4833	10055	415	1248	1213	2.5e-123

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
GTP cyclohydrolase II, / 3, 4-dihydroxy-2-butanone 4-phosphate synthase, ribA:ribA protein	pir:C70331	C70331

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4881507_c3_439	4834	10056	960	2880	929	3.2e-93

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
51.7.31.92_c3_419.....	4835	10057	611	1836	1321	9.1e-135

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YDCP_ECOLI	

Description

PUTATIVE PROTEASE YDCP PRECURSOR,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
52.5.9.8.3.8_f1_9.....	4836	10058	707	2124	123	3.9e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
heme receptor	gp:VIBHUTA	L27149

Description

Vibrio cholerae heme receptor (hutA) gene, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5272312_c2_350	4837	10059	120	363	88	0.0018

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein Rv0587	pir:F70907	F70907

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5275425_f2_134	4838	10060	81	246		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5290912_f3_221	4839	10061	124	375		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5880050_c3_414	4840	10062	111	336		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6366576_f1_13	4841	10063	65	198		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6367805_f3_272	4842	10064	212	639	96	0.010

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
outer membrane protein 21, Omp21	gp:CAAJ1918	AJ001918

Description

Comamonas acidovorans omp21 gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6417192_c3_420	4843	10065	72	219		

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13757180_f1_23	4844	10066	60	183	70	0.033

hypothetical protein APE1598 pir:A72539 A72539

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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16.5.3.5.8.3.0...1.3...5.9..... 4843 10007 51 73 51

Protein name Locus Name Accession No.

ANSWER

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16603402_c2_78	4846	10068	337	1014	943	1.0e-94
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
WbnF				gp:AF172324	AF172324	
<u>Description</u>						

Escherichia coli GalF (galF) gene, partial cds; O-antigen repeatunit transporter Wzx (wzx), WbnA (wbnA), O-antigen polymerase Wzy(wzy), WbnB (wbnB), WbnC (wbnC), WbnD (wbnD), WbnE (wbne), UDP-Glc-4-epimerase GalE (gale), 6-phosphogluconate dehydrogenaseGnd (gnd), UDP-Glc-6-dehydrogenase Uqd (uqd), and WbnF (wbnF)genes, complete cds; and chain length determinant

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21.6.7.8.5.0.0_c1_64.....	4847	10069	474	1425	1297	3.2e-132
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
3-isopropylmalate dehydratase, large chain			pir:T29083			T29083
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23.6.31.6.2.7_c2_74.....	4848	10070	201	606	462	9.7e-44
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
sp:LEUD_HAEIN			P44438			
<u>Description</u>						

(ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23.6.34.42.5_c1_66.....	4849	10071	357	1074	1836	2.4e-189
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
sp:LEU3_BACFR			P54354			
<u>Description</u>						

(IMDH) (3-IPM-DH)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24270450_c1_67	4850	10072	528	1587	216	2.0e-14
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
unknown				gp:AF036677	AF036677	
<u>Description</u>						

Salmonella typhimurium putative operon regulated by PmrAB, necessary for 4-aminoarabinose lipid A modification and polymyxin resistance, PmrG (pmrG) gene, partial cds; PmrF (pmrF) gene and 6orfs, complete cds; and PmrD (pmrD) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24335131_f1_25	4851	10073	63	192	106	5.1e-06
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
hypothetical protein PH0219				pir:A71245	A71245	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24337765_c1_68.....	4852	10074	1032	3096	617	2.6e-86
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
115K outer membrane protein precursor:SusC protein				pir:JC6027	JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
282708_f2_42.....	4853	10075	60	183		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
NO-HIT				pir:JC6027	JC6027	
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34081405_c2_71	4854	10076	88	267	110	1.9e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PHS004	pir:F71245	F71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34407837_c2_73	4855	10077	500	1503	1207	1.1e-122

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:LEU1_HAEIN	P43861

Description

SYNTHASE) (ALPHA-IPM SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4805262_c1_65	4856	10078	512	1539	666	2.3e-65

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
2-isopropylmalate synthase (leuA-1) homolog	pir:E69369	E69369

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5332506_f1_24	4857	10079	95	288	73	0.034

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PH0220	pir:B71245	B71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5867141_c3_83	4858	10080	218	657	232	2.0e-18

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
lipid A disaccharide synthase	pir:B72014	B72014

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5901877_c2_76	4859	10081	269	810	366	1.4e-33

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
dolichol-phosphate mannosyltransferase	pir:G70463	G70463

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5.5.5.1_t3_46	4860	10082	86	261		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10164677_c2_249	4861	10083	154	465	170	1.7e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
proline-rich protein precursor	pir:S23737	S23737

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10241436_t1_8	4862	10084	142	429		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1236.0.0.2_c2_228	4863	10085	169	510	111	1.4e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
arabinogalactan-like protein	pir:S52994	S52994

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12500183_f2_42	4864	10086	128	387	124	4.4e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein Rv3864	pir:E70656	E70656

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
125037_f1_34	4865	10087	687	2064	439	3.2e-40

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (Raga)	gp:PGI130872	AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13000040_f3_115	4866	10088	332	999		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13069511_f2_47	4867	10089	121	366		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13956536_c1_183	4868	10090	431	1296		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14587753_c2_217	4869	10091	325	978	270	4.5e-22

Protein name Locus Name Acc#

sp:TRC4_ECOLI

Description

DNA PRIMASE TRAC, (REPLICATION PRIMASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14727281_f2_72	4870	10092	119	360	98	5.8e-05

Protein name Locus Name Acc#

sp:DH18_ARATH P30185

Description

DEHYDRIN RAB18

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15032692_c1_162	4871	10093	220	663	101	0.036

Protein name Locus Name Acc#

exodeoxyribonuclease V, gamma chain (recC) homolog pir:A70179 A70179

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20260_f3_137	4872	10094	589	1770	89	0.041

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:U96771	U96771

Description

Prevotella bryantii putative polygalacturonase, B-1, 4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20506501_c2_202	4873	10095	269	810	235	1.1e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein b1488	pir:C64902	C64902

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20594841_f3_117	4874	10096	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2119013_c1_147	4875	10097	400	1203	115	1.5e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein SC6G4.36c SC6G4.36c	pir:T35587	T35587

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21507338_f1_11	4876	10098	736	2211	559	2.3e-89

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:BFU63096	U63096

Description

Bacteroides fragilis (bctA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21578375_c1_197	4877	10099	776	2331	197	3.2e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:AF083424	AF083424

Description

Ateline herpesvirus 3 complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22548191_f2_51.....	4878	10100	177	534	122	5.2e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein T15B7.3	pir:T32250	T32250

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
229.06.5.06_c3_30.9.....	4879	10101	882	2649	315	5.4e-25

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
mobilization protein C	gp:AF118243	AF118243

Description

Bacteroides fragilis mobilization protein C (mobC) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23486336_c1_146	4880	10102	77	234	63	0.0098

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
R07E5.1 protein (clone R07E5)	pir:S43604	S43604

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2350306_c1_144	4881	10103	100	303	111	1.5e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein PH0217	pir:G71244	G71244

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23860937_c2_219	4882	10104	186	561	149	1.4e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YPSA_BACSU	P50838

Description

HYPOTHETICAL 21.1 KD PROTEIN IN COTD-KDUD INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2426563.7_f1_12	4883	10105	131	396		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24480382_f1_35	4884	10106	154	465		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

<u>NO-HIT</u>

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24489062_f3_120	4885	10107	286	861		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24504062_f1_14	4886	10108	211	636		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24642200_c2_262	4887	10109	192	576		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24693836_c2_230	4888	10110	191	576		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25589017_c1_192	4889	10111	233	702		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25627153_f3_143	4890	10112	74	222		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25878812_f1_10	4891	10113	109	330	85	0.0044

Protein name Locus Name Acc#

antigen 5401 pir:A60643 A60643

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26442203_f3_104	4892	10114	278	837	125	2.0e-05

Protein name Locus Name Acc#

chromosome partitioning ATPase Soj pir:D75570 D75570

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26752162_f2_60	4893	10115	213	642		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26751662_f2_71	4894	10116	359	1080		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29354192_c2_253	4895	10117	349	1050	79	0.027

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:S83195	S83195

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3136318_c1_189	4896	10118	226	681	108	2.3e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
sperm mitochondrial capsule selenoprotein	pir:A37199	A37199

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31423591_f1_17.....	4897	10119	116	351	116	7.5e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
major ampullate fibroin protein	pir:A36068	A36068

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31432007_c2_234.....	4898	10120	101	306	118	3.8e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
KIAA0775 protein	gp:AB018318	AB018318

Description

Homo sapiens mRNA for KIAA0775 protein, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31836561_c1_166	4899	10121	596	1791	313	3.1e-27

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:CBGIDPAB	Y10436

Description

C.burnetii put. genes for encoding glucose inhibited divisionprotein A and B.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33398568_c1_145	4900	10122	78	237		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.3.7.92215....f2...67.....	4901	10123	457	1374		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.4.11.98.41....f2...54.....	4902	10124	240	723	111	0.00096

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>troponin T</u>	<u>pir:S02708</u>	<u>S02708</u>
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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34181583_f3_116	4903	10125	194	585		
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Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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34407575_f1_20	4904	10126	155	468		
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Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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34413942_f2_55	4905	10127	101	306		
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Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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34473416_c2_223	4906	10128	251	756		
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Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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34495965_f1_31	4907	10129	110	333		
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Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34652032_f3_107	4908	10130	407	1224	162	3.0e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical 119.5K protein (uvrA region) :ORF 1 protein	pir:JQ0405	JQ0405

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.523.945.8_c1_17.9	4909	10131	134	405	100	3.5e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
latent nuclear antigen	gp:AF083501	AF083501

Description

Macaca mulatta rhabdovirus 17577 R1, dihydrofolate reductase, complement binding protein, ssDNA binding protein, transportprotein, glycoprotein B, DNA polymerase, R2, thymidylate synthase, R3, Bcl-2 homolog, capsid protein, tegument protein, thymidinekinase, glycoprotein H, major capsid protein, capsid protein, kinase, alkaline exonuclease, glycoprotein M,
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.526.756.7_c3_29.9	4910	10132	476	1431	89	0.0035

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
beta-D-galactosidase	gp:BRPLACZ01	M63097

Description

Brugia malayi beta-D-galactosidase (lacZ) mRNA, partial cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.6.0.6.734.3_c3_3.0.8	4911	10133	286	861	179	9.1e-12

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
MocB (Tn4399)	pir:B48487	B48487

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36150277_c1_164	4912	10134	65	198		

Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36442965_c3_27.0.....	4913	10135	69	210	63	0.014

Protein name Locus Name

Acc#

envelope protein gp:HTVENVHE M61052

Description

Human T-cell leukemia virus I (HTLV1) envelope (env) gene, 5' end.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36509443_f3_131.....	4914	10136	684	2055	375	1.7e-31

Protein name Locus Name

Acc#

hypothetical protein Slrl135 pir:S77439 S77439

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36520337_c1_196.....	4915	10137	132	399		

Protein name Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
400767_c3_284.....	4916	10138	168	507	228	6.1e-19

Protein name Locus Name

Acc#

DNA repair protein RadC pir:C70439

C70439

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4027135_f3_110	4917	10139	337	1014		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5.0.0925_c3_266.....	4918	10140	442	1329	867	1.2e-86
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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transposase	gp:AF038866	AF038866
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Description

Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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593.752_f1_16.....	4919	10141	104	315	81	6.7e-05
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein	pir:B40505	B40505
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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8.13.902_f3_132.....	4920	10142	112	339	83	0.0034
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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putative resolvase	gp:DASOR	
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Description

Desulfurolobus ambivalens tnpA, tnpB, rfbD and sor genes and ORF2, ORF3, ORF4 and ORF5.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12944067_f2_4	4921	10143	334	1005		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4095192_f1_1.....	4922	10144	309	930		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1226.063...c3_5.....	4923	10145	174	522		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
183...c1_18.....	4924	10146	425	1278	1208	8.6e-123

Protein name Locus Name Acc#

sp:KBL_ECOLI P07912

Description

(GLYCINE ACETYLTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25783462_f1_7	4925	10147	244	735		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34181515_f2_8	4926	10148	349	1050		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5189062_c2_27	4927	10149	139	420	77	0.018

Protein name Locus Name Acc#

hypothetical protein PH0778 pir:D71126 D71126

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5257762_f2_9	4928	10150	309	930	106	0.0078

Protein name Locus Name Acc#

gp:D42067 D42067

Description

Porphyromonas gingivalis DNA for Fimbrillin, ORF1-4, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
676887_f1_5	4929	10151	68	207	130	1.5e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:VCH231106	AJ231106

Description

Vibrio cholerae z47f gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
785285_f2_11	4930	10152	324	975	570	3.5e-55

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein F08F3.4	pir:T29433	T29433

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10757933_f2_49.....	4931	10153	589	1770	107	3.4e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:U96771	U96771

Description

Prevotella bryantii putative polygalacturonase, B-1, 4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10938205_c1_106.....	4932	10154	1060	3183	565	1.8e-57

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
beta-N-Acetylglucosaminidase	gp:AB008771	AB008771

Description

Streptomyces thermophilus nagA gene for beta-N-Acetylglucosaminidase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14657927_f3_70	4933	10155	242	729	563	1.9e-54

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:Y796_METJA	Q58206

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0796

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
17010202_f2_40	4934	10156	148	447	218	1.5e-17

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein MTH695	pir:F69192	F69192

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19953.05_f3_73.....	4935	10157	261	786	214	1.8e-17

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
RNA polymerase sigma factor SigZ-like protein	gp:AF137263	AF137263

Description

Bacteroides thetaiotaomicron 30S ribosomal protein S16-like protein, fucose gene cluster, and RNA polymerase sigma factor SigZ-like protein (sigZ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19972.762_c2_124.....	4936	10158	1007	3024	566	5.9e-58

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
beta-N-Acetylglucosaminidase	gp:AB008771	AB008771

Description

Streptomyces thermophilic nagA gene for beta-N-Acetylglucosaminidase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
212757_c1_80	4937	10159	466	1401	247	8.9e-24

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp: MUTS_THEAQ	Q56215

Description

DNA MISMATCH REPAIR PROTEIN MUTS

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21681502_f3_74	4938	10160	310	933	200	3.2e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transmembrane sensor	gp: AF051691	AF051691

Description

Pseudomonas aeruginosa stress factor A (psfA), ECF sigma factor (fiuI), transmembrane sensor (fiuR), and hydroxamate-typeferrisiderophore receptor (fiuA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23475053_f1_20.....	4939	10161	1085	3258	583	1.8e-93

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
receptor antigen (RagA)	gp: PGI130872	AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24072250_c3_154.....	4940	10162	343	1032	512	4.9e-49

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glucose kinase	gp: BMGLUCKIN	AJ000005

Description

Bacillus megaterium glk gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24651537_f2_41	4941	10163	368	1107	156	3.4e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein slr1207	pir:S77541	S77541

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25557818_f2_42	4942	10164	450	1353	662	6.2e-65

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
immunoreactive 51kD antigen PG52	gp:AF175719	AF175719

Description

Porphyromonas gingivalis strain W50 immunoreactive 51kD antigenPG52 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26.6.00932_f1_17	4943	10165	119	360	299	1.8e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:RL19_STRTR	034031

Description

50S RIBOSOMAL PROTEIN L19

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26.7.027_f1_26	4944	10166	117	351	86	0.027

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein BB0794	pir:A70199	A70199

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26750178_c1_104	4945	10167	266	801	199	5.1e-15

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
UDP-sugar hydrolase	pir:A72201	A72201

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.16.3.3.92_c2_51	4946	10168	724	2175	1095	8.1e-111

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
melibiase	gp:TEMELA	Y08557

Description

T.ethanolicus melA and lacA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.59.7.8253_c2_129	4947	10169	1029	3087	454	2.3e-73

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4.115.9.27_c1_81	4948	10170	202	609		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>				
4305138_f1_22	4949	10171	538	1617	156	9.3e-14				
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>					
alpha-xylosidase			pir:A72394		A72394					
<u>Description</u>										
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>				
4409540_f2_39	4950	10172	436	1311	305	4.2e-27				
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>					
conserved hypothetical protein yknZ			pir:E69858		E69858					
<u>Description</u>										
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>				
5.086.542_f1_19	4951	10173	280	843	226	3.0e-18				
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>					
hypothetical protein			pir:S76946		S76946					
<u>Description</u>										
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>				
52.734.38_f3_76	4952	10174	183	552	150	1.8e-09				
<u>Protein name</u>			<u>Locus Name</u>		<u>Acc#</u>					
putative alpha-glucosidase			gp: AAC252161		AJ252161					
<u>Description</u>										
Alicyclobacillus acidocaldarius maltose/maltodextrine transport gene region (maleFGR genes, cdaA gene and glcA gene).										

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5339381_F3_75	4953	10175	116	351	157	3.1e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative alpha-glucosidase	gp: AAC252161	AJ252161

Description

Alicyclobacillus acidocaldarius maltose/maltodextrine transport gene region
(maleFGR genes, cdaA gene and glcA gene).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
822127_c1_105	4954	10176	291	876	328	6.1e-29

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp: 5NTD_DISOM	P29240

Description

5'-NUCLEOTIDASE PRECURSOR, (ECTO-NUCLEOTIDASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
I0345327_c2_2	4955	10177	114	345	266	1.2e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
115K outer membrane protein precursor: SusC protein	pir:JC6027	JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
I3099158_c3_48	4956	10178	118	357		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16589717_c2_28	4957	10179	301	906	167	2.2e-09

Protein name Locus Name Acc#
gp:MMSAG X84710

Description

M.mazei surface antigen genes orf492, orf375 and orf783.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24024182_f3_13	4958	10180	311	936		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24068841_c3_46.....	4959	10181	281	846		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25422331_c3_47.....	4960	10182	518	1557		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26370887_c3_45	4961	10183	179	540		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29511635_c3_44	4962	10184	106	321	84	0.0076

Protein name Locus Name Acc#

hypothetical protein BB0212 pir:D70126 D70126

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.001566_f3_12	4963	10185	318	957	103	0.024

Protein name Locus Name Acc#

probable chitinase pir:T42071 T42071

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.2040953_c1_22	4964	10186	64	195		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.5143_f3_14	4965	10187	624	1875	371	1.6e-44

Protein name Locus Name Acc#

otnA protein pir:S70958 S70958

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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6495337_f1_1	4966	10188	132	399		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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13100885_f1_1.....	4967	10189	316	951	129	2.4e-05
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Protein name

Locus Name

Acc#

hypothetical protein s1r1515

pir:S75464

S75464

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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1219538_c2_95.....	4968	10190	508	1527	195	7.9e-17
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Protein name

Locus Name

Acc#

unknown

gp:U96771

U96771

Description

Prevotella bryantii putative polygalacturonase, B-1,4-endoglucanase, and mannanase genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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13672753_c2_88.....	4969	10191	572	1719	613	9.7e-60
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Protein name

Locus Name

Acc#

carboxyl-terminal proteinase

pir:F70369

F70369

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14492660_c2_98	4970	10192	71	213		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14631626_f3_55	4971	10193	149	450		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23548552_c2_90	4972	10194	772	2319	3902	0.0

Protein name Locus Name Acc#

beta-glucosidase gp:AF006658 AF006658

Description

Bacteroides fragilis beta-glucosidase gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24806576_c2_89	4973	10195	948	2847	104	7.9e-05

Protein name Locus Name Acc#

unknown gp:AF124349 AF124349

Description

Zymomonas mobilis ZM4 fosmid clone 41A4, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26385883_c3_101	4974	10196	360	1083	419	3.5e-39
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
				sp:YZ37_SYN3		Q55480

Description

HYPOTHETICAL SUGAR KINASE SLR0537

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33242062_c3_100	4975	10197	824	2475	802	8.8e-82
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
hypothetical protein TM0280				pir:F72395		F72395

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33864378_c1_78.....	4976	10198	1009	3030	432	1.3e-92
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
receptor antigen (RagA)				gp:PGI130872		AJ130872

Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4413377_c2_97.....	4977	10199	576	1731	136	5.4e-06
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
				sp:XYNB_PRERU		P48791

Description

1,4-BETA-XYLOSIDASE) (EXO-BETA-(1,4)-XYLANASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4961578_c2_86	4978	10200	514	1545		
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Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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984512_c2_96.....	4979	10201	437	1314		
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Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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15797080_f3_1.....	4980	10202	113	342		
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Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24806591_c1_2.....	4981	10203	89	267	226	6.0e-18
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Protein name Locus Name Acc#

SP:YNHE_ECOLI

P77522

Description

HYPOTHETICAL 56.3 KD PROTEIN IN LPP-AROD INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25815841_c3_4	4982	10204	77	234	223	2.1e-18

Protein name Locus Name Acc#
 probable oxidoreductase pir:T34993 T34993

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11854168_f3_1	4983	10205	187	564	317	2.2e-28

Protein name Locus Name Acc#
 4-methyl-5(*b*-hydroxyethyl)-thiazole monophosphate biosynthesis protein (thiJ) homolog pir:D70177 D70177

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21595663_c2_2	4984	10206	134	402	200	1.3e-14

Protein name Locus Name Acc#
 115K outer membrane protein precursor: SusC protein pir:JC6027 JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10944505_f3_7	4985	10207	70	213		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13707938_f1_1	4986	10208	374	1125	106	0.0014

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
omp85 analog	pir:D72094	D72094

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
17.07.03.00_g3_15	4987	10209	69	210		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24431268_f2_5	4988	10210	187	564		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25.786.06.7_f3_8	4989	10211	68	207	104	0.00010

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YJDB_ECOLI	

Description

HYPOTHETICAL 61.7 KD PROTEIN IN BASS-ADIV INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32031466_f1_3	4990	10212	133	402	100	0.00026

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YBIP_ECOLI	P75785

Description

HYPOTHETICAL 59.7 KD PROTEIN IN OMPX-MOEB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10635006_f1_1	4991	10213	107	324		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23475780_c2_2.....	4992	10214	288	864		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23991662_f1_1.....	4993	10215	210	633	553	2.2e-53

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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mobilization protein A	gp:AF118241	AF118241
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Description

Bacteroides fragilis mobilization protein A (mobA) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12541385_c2_36	4994	10216	104	312		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20588187_c2_30	4995	10217	276	831	91	0.047

Protein name Locus Name Acc#

polymorphic outer membrane protein G family gp:AB033794 AB033794

Description

Chlamydophila pneumoniae pmp_3.1 gene for polymorphic outermembrane protein G family, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21914762_c2_32	4996	10218	61	186		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22265701_f2_8	4997	10219	495	1488		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24641877_c3_38	4998	10220	115	348		
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Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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25597781_c3_40.....	4999	10221	555	1668		
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Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4110090_c3_37.....	5000	10222	358	1077	104	0.032
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Protein name Locus Name Acc#

hypothetical protein Y26D4A.9 pir:T26569 T26569

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5164042_c1_28.....	5001	10223	209	630		
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Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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15911275_c1_24.....	5002	10224	337	1014		
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Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26368757_c2_29	5003	10225	126	381		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2736657_c2_31	5004	10226	71	216		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
49.00250_f3_17	5005	10227	708	2127	929	3.3e-178

Protein name Locus Name Acc#

conserved hypothetical protein ydcl pir:G69773 G69773

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6.054.083_c2_36	5006	10228	108	324	75	0.0099

Protein name Locus Name Acc#

E3 class 2 protein pir:B46308 B46308

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6.28.581.7_c3_37	5007	10229	277	834		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14882768_f3_29	5008	10230	304	912	587	5.5e-57

Protein name Locus Name Acc#

conserved hypothetical protein yisQ pir:H69837 H69837

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15.042.062_f3_25	5009	10231	257	774	213	2.4e-17

Protein name Locus Name Acc#

gp:SPU59236 U59236

Description

Synechococcus PCC7942 ribosomal protein S1 of 30S ribosome (rps1), ORF271, ORF231, ORF341, carboxyltransferase alpha subunit (accA), ORF245, ORF227, and GTP cyclohydrolase I (folE) genes, completecds, and ORF205 gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16.8.296.37_f3_23	5010	10232	118	357	213	2.4e-17

Protein name Locus Name Acc#

sp:YEBR_ECOLI

Description

HYPOTHETICAL 20.3 KD PROTEIN IN PRC-PPHA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24.8.0.063_c3_62	5011	10233	66	201		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25943937_f3_28	5012	10234	152	459		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29473527_f1_1	5013	10235	160	483	198	1.8e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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two component sensor	gp:AF030352	AF030352
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Description

Pseudomonas aeruginosa two component sensor (lemA) gene, partialcds.						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3398391_f3_27	5014	10236	463	1392	414	1.2e-38

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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conserved hypothetical protein	pir:G72220	G72220
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3947162_f3_22	5015	10237	583	1752	540	5.3e-52

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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2',3'-cyclic-nucleotide 2'-phosphodiesterase, precursor	pir:H64532	H64532
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4477328_f2_13	5016	10238	112	339		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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496.0936..f1..7	5017	10239	766	2301	252	7.1e-18
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Protein name

Locus Name

Acc#

sp:CIRA_ECOLI	P17315
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Description

COLICIN I RECEPTOR PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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86.037..cl..32	5018	10240	224	675		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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131.05192..c3..22	5019	10241	653	1962		
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Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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26369015_c2_21	5020	10242	840	2520	440	7.4e-74
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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115K outer membrane protein precursor: SusC protein	pir:JC6027	JC6027
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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44.08275_c3_23.....	5021	10243	62	189		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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25.8.32158_f1_1.....	5022	10244	191	576	475	4.1e-45
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein jhp0042	pir:H71981	H71981
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3.3.82312_f1_1.....	5023	10245	202	609	127	1.3e-05
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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TonB-dependent receptor HmuR	gp:PGU87395	U87395
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Description

Porphyromonas gingivalis TonB-dependent receptor HmuR (hmuR) gene, complete cds.						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1038140_f1_2	5024	10246	1095	3288		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10585927_f1_12	5025	10247	89	270		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10979687_c3_125	5026	10248	136	411	330	9.4e-30

Protein name Locus Name Acc#

sp:MSCL_ERWCA 068284

Description

LARGE-CONDUCTANCE MECHANOSENSITIVE CHANNEL

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11751442_f1_1	5027	10249	93	282		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13017676_c1_85	5028	10250	176	531	133	1.2e-07

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
trsl protein (tral)	gp:AE001272	AE001272

Description

Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmid sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13781250_c2_106	5029	10251	67	204	202	3.5e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein 1	pir:I40237	I40237

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13.932825_f3_50.....	5030	10252	721	2166	121	0.00075

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:T7CG	

Description

Genome of bacteriophage T7.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14315933_c1_75.....	5031	10253	140	423		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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16531331_c3_128	5032	10254	292	879	90	0.00059
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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ras interacting protein RIPA	gp:AF159241	AF159241
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Description

Dictyostelium discoideum ras interacting protein RIPA (ripA) mRNA, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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23636550_f2_25	5033	10255	281	846	154	7.3e-10
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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tetracycline resistance element mobilization regulatory protein rtec	pir:A36927	A36927
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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236.74130...c2...107.....	5034	10256	415	1248	137	5.2e-06
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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clostripain-related protein	pir:B72351	B72351
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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239.54136...c2...119.....	5035	10257	85	258		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24641637_c2_103	5036	10258	232	699	485	3.5e-46

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:AQPZ_ECOLI	

Description

AQUAPORIN Z (BACTERIAL NODULIN-LIKE INTRINSIC PROTEIN)
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24645261_c3_132	5037	10259	378	1137	395	1.2e-36

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YHCG_ECOLI	P45423

Description

HYPOTHETICAL 43.3 KD PROTEIN IN GLTF-NANT INTERGENIC REGION (O375)
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
253.7562_c1_6.9.....	5038	10260	120	363		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26.594087_f2_26.....	5039	10261	138	417		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32317217_f1_4	5040	10262	143	432		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32442125_c1_70.....	5041	10263	235	708	170	1.8e-13

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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immunoreactive 42kD antigen PG33	gp:AF175715	AF175715
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Description

Porphyromonas gingivalis strain W50 immunoreactive 42kD antigenPG33 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32453507_c1_74.....	5042	10264	91	276	76	0.023

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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elongation factor Ts	gp:AF195952	AF195952
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Description

Phaeodactylum tricornutum ribulose-1,5-bisphosphatecarboxylase/oxygenase large subunit (rbcL), ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit (rbcS), and elongation factor Ts (EF-Ts) genes, complete cds;chloroplast genes for chloroplast products.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33397331_c3_126.....	5043	10265	87	264		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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35292938_f3_53	5044	10266	143	432		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>		
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NO-HIT		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4116262_c2_10.5.....	5045	10267	98	297	169	1.1e-12
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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DNA-binding protein, HU	pir:H72396	H72396
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<u>Description</u>		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4159811_c1_93.....	5046	10268	81	246		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>		
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NO-HIT		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5110942_c2_109.....	5047	10269	546	1641	912	2.0e-91
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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DNA topoisomerase III topB	pir:H69724	H69724
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<u>Description</u>		
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5250000_c2_108	5048	10270	517	1554	178	4.0e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
high molecular weight glutenin subunit	gp:ASU39229	U39229

Description

Aegilops tauschii high molecular weight glutenin subunit (Glu-1-2) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5895187_f1_5	5049	10271	165	498		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6.5.25.28.6....f2...3.0.....	5050	10272	69	210		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1.3.8.6.9.0.0.3....f3....3.....	5051	10273	163	492	183	3.6e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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unknown gp:AF048749 AF048749

Description

Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>					
22469452_f3_2	5052	10274	174	525	174	3.2e-13					
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>						
unknown				gp:AF048749	AF048749						
<u>Description</u>											
Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.											
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>					
34266886_c1_4	5053	10275	122	369							
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>						
<u>Description</u>											
NO-HIT											
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>					
7.81932_f1_1	5054	10276	308	927	528	9.5e-50					
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>						
115K outer membrane protein precursor: SusC protein					pir:JC6027	JC6027					
<u>Description</u>											
<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>					
236.3188.7_c3_5	5055	10277	268	807	151	1.0e-08					
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>						
sp: HOLB_HAEIN					P43748						
<u>Description</u>											
DNA POLYMERASE III, DELTA' SUBUNIT,											

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16445326_f3_22	5056	10278	73	222		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
166.0.3.3.77..f2..15.....	5057	10279	559	1680	122	0.00036

Protein name Locus Name Acc#

carboxyl-terminal proteinase
ctpB:hypothetical protein slr0257:hypothetical
protein slr0257

pir:S74579

S74579

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
18.7540..c2..3.2.....	5058	10280	171	516		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
244.126.32..c3..3.5.....	5059	10281	84	255		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648941_c3_41	5060	10282	498	1494	755	8.7e-75

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
putative TonB-dependent outer membrane receptor	gp:AF048749	AF048749

<u>Description</u>
Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25785191_c3_34	5061	10283	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>
NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2.945.33.75_c1_26.....	5062	10284	65	198		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>
NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2.9.7.3.93.75_c1_25.....	5063	10285	931	2796	136	0.00047

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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<u>Description</u>		
hypothetical protein PFB0540w	pir:D71612	D71612

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3145252_c1_24	5064	10286	278	837	139	1.3e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:APRF_PSEAE	Q03027

Description

ALKALINE PROTEASE SECRETION PROTEIN APRF
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35194686_f3_23	5065	10287	249	750		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4.33.5.962_c3_40.....	5066	10288	228	687	92	0.0096

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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putative HSP20	gp:AF072875	AF072875
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Description

Mycobacterium smegmatis putative HSP20 (hsp) gene, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4.8.92140_c3_39.....	5067	10289	475	1428	134	2.2e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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ORF MSV261 leucine rich repeat gene family	gp:AF063866	AF063866
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Description

Melanoplus sanguinipes entomopoxvirus, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10429567_f3_3	5068	10290	77	234		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4103575_f3_4	5069	10291	394	1185	514	1.3e-54

Protein name Locus Name Acc#

115K outer membrane protein precursor:SusC protein

pir:JC6027

JC6027

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10995166_f2_44	5070	10292	63	192		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14665963_f2_30	5071	10293	393	1182	255	4.8e-20

Protein name Locus Name Acc#

conserved hypothetical protein

pir:H72273

H72273

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16676688_f1_1	5072	10294	492	1479	646	3.1e-63

Protein name Locus Name Acc#

conserved hypothetical protein yngK

pir:H69893

H69893

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21521937_c1_70	5073	10295	301	906	231	2.9e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:SCRK_SALTY	P26984

Description

FRUCTOKINASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24023457_f3_52	5074	10296	768	2307	373	8.2e-31

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:LEMA_PSESY	P48027

Description

SENSOR PROTEIN LEMA,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24298262_c1_74.....	5075	10297	282	849	752	1.8e-74

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:PROW_ECOLI	P14176

Description

GLYCINE BETAINE/L-PROLINE TRANSPORT SYSTEM PERMEASE PROTEIN PROW
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
244.783.88_c2_101.....	5076	10298	285	858	453	8.7e-43

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
glycine-betaine binding permease protein	gp:AF139575	AF139575

Description

Lactococcus lactis BusAA (busAA) and glycine-betaine binding permease protein (busAB) genes, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24644706_c1_71	5077	10299	909	2730	391	2.7e-55

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hybrid histidine kinase	gp:AF029704	AF029704

Description

Dictyostelium discoideum hybrid histidine kinase (dhkD) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648432_f1_10	5078	10300	214	645		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2466.0817_c3_113.....	5079	10301	281	846	1490	1.1e-152

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
fructanase	pir:A36915	A36915

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26597136_c3_114.....	5080	10302	390	1173	268	1.3e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:GLUP_BRUAB	Q44623

Description

GLUCOSE/GALACTOSE TRANSPORTER

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2817217_c1_72	5081	10303	124	375	210	4.9e-17

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YBAZ_ECOLI	P75707

Description

HYPOTHETICAL 14.4 KD PROTEIN IN TESB-HHA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30084532_c2_100	5082	10304	412	1239	1028	1.0e-103

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ATPase homolog GbuA	gp:AF039835	AF039835

Description

Listeria monocytogenes ATPase homolog GbuA (gbuA), putative glycinebetaine membrane transport protein GbuB (gbuB), and putative glycine betaine binding protein GbuC (gbuC) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
356.813.08..f1..14.....	5083	10305	102	309	125	5.0e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein APE2061	pir:G72510	G72510

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
429511..f2..31.....	5084	10306	192	579	132	9.0e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein	pir:G75555	G75555

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4712825_c1_88	5085	10307	398	1197		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5477752_f1_9.....	5086	10308	1193	3582	3762	0.0

Protein name _____ Locus Name _____ Acc# _____

pyruvate ferredoxin oxidoreductase gp:CPA17727 Y17727

Description

Clostridium pasteurianum genes encoding putative pyruvateferredoxin oxidoreductase (8005 bp).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2031461_c2_5.....	5087	10309	281	846	150	1.8e-08

Protein name _____ Locus Name _____ Acc# _____

hypothetical protein aq_1477 pir:D70428 D70428

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32431880_f2_1.....	5088	10310	280	843		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21562667_f1_4	5089	10311	617	1854	2041	4.6e-211
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
	sp:ILVD_HAEIN					

Description

DIHYDROXY-ACID DEHYDRATASE, (DAD)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23712785_f2_10	5090	10312	569	1710	1245	1.0e-126
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
	acetolactate synthase, large subunit					

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31908538_f2_7	5091	10313	235	708		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35204656_f1_6	5092	10314	80	240	64	0.0053
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
	capsid portal protein					

Description

Bacteriophage 186, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4822001_f3_12	5093	10315	718	2157	269	2.4e-20

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:AF083424	AF083424

Description

Ateline herpesvirus 3 complete genome.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6678425_f2_9	5094	10316	397	1194		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23.516.942...c3...5.....	5095	10317	305	915		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25.6.6.7.6.31...c2...3.....	5096	10318	83	252	131	1.4e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:Y052_BORBU	051081
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Description

HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE BB0052,
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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2442257_f1_1	5097	10319	80	243		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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2628.96.5.0_f1_3	5098	10320	140	423	257	5.1e-22
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:YM64_ARCFU	028020
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Description

HYPOTHETICAL PROTEIN AF2264

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3.1913.93.3_c3_27	5099	10321	304	915		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4164.011_f3_8	5100	10322	320	963	377	9.9e-35
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:YXEH_BACSU	P54947
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Description

HYPOTHETICAL 30.2 KD PROTEIN IN IDH-DEOR INTERGENIC REGION
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6444402_f2_5	5101	10323	495	1488	1190	7.0e-121

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
cysteinyl-tRNA synthetase	pir:A75368	A75368

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12125931_f2_4	5102	10324	214	645	220	4.3e-18

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase-related protein	pir:H72245	H72245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12988762_f2_5	5103	10325	62	189		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2813942_f2_3	5104	10326	73	222		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12944677_c2_5	5105	10327	453	1359	302	7.3e-35

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
TonB-dependent receptor HmuR	gp:PGU87395	U87395

Description

Porphyromonas gingivalis TonB-dependent receptor HmuR (hmuR) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22850381_c1_4	5106	10328	77	234		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14664017_c3_4	5107	10329	210	630	379	9.1e-34

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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receptor antigen (RagA)	gp:PGI130872	AJ130872
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Description

Porphyromonas gingivalis W50 receptor antigen (rag) locus encoding a major immunodominant 55kDa antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20164665_f1_1	5108	10330	68	207	51	0.0055

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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50kDa lectin	gp:BMO50KDAL	D14168
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Description

Silk worm mRNA for 50kDa lectin, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2460837_f3_2	5109	10331	614	1845	556	9.9e-54

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
adenylylate cyclase homolog	pir:T17197	T17197

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14923563_c1_10	5110	10332	145	438		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15742327_f1_2	5111	10333	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24398917_c1_11	5112	10334	193	582	302	8.7e-27

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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conserved hypothetical protein	pir:G72380	G72380
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33772907_c2_15	5113	10335	117	354	71	0.026

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
HdcB	gp:OO058865	U58865

Description

Oenococcus oeni histidine decarboxylase (hdcA) gene, complete cds; and HdcB (hdcB) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35267037_c2_16	5114	10336	117	354		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16.5.4.10.0.3....f3....3.....	5115	10337	64	195		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20.5.0.0.6.5.7....f3....4.....	5116	10338	515	1548	1069	4.6e-108

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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inorganic pyrophosphatase	gp:D88820	D88820
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Description

Acetabularia mediterranea mRNA for inorganic pyrophosphatase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10944500_c2_9	5117	10339	299	900	341	6.4e-31

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:PIGUFMR	M30284

Description

Pig uteroferrin mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
834393_f1_1	5118	10340	163	492	407	6.5e-38

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:S76672	S76672

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1987750_f2_4	5119	10341	333	1002		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23704675_c3_10	5120	10342	300	903	1106	5.5e-112

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
heat shock protein 60	gp:BFO6516	AJ006516

Description

Bacteroides forsythus groEL gene, strain ATCC 43037.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4022312_c3_9	5121	10343	93	282	393	2.0e-36

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:CH10_PORGI	P42376

Description

10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES)
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10394667_f2_16	5122	10344	123	372		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14496.03.0_f1_8.....	5123	10345	227	684		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15742327_c2_71.....	5124	10346	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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19562800_f2_14	5125	10347	327	984		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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19814057_f1_7	5126	10348	224	675		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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23438557_f1_13	5127	10349	397	1194		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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23554057_f1_10	5128	10350	75	228	71	0.039
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:UCRH_YEAST

P00127

Description

(MITOCHONDRIAL HINGE PROTEIN) (COMPLEX III POLYPEPTIDE VI)						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24024067_f1_5	5129	10351	810	2433	224	2.5e-28

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	gp:BFU63096	U63096

Description

Bacteroides fragilis (bctA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24398917_f3_50	5130	10352	193	582	304	5.4e-27

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein	pir:G72380	G72380

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24648436_f1_3.....	5131	10353	204	615		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
253783_c1_64.....	5132	10354	73	222		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25442675_f1_4	5133	10355	140	423		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25633287_f1_9	5134	10356	62	189		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25633312_f3_47	5135	10357	434	1305		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26568908_f3_30	5136	10358	154	465		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26758568_f3_43	5137	10359	283	852	94	0.045

Protein name _____ Locus Name _____ Acc# _____

H+-transporting ATP synthase, protein 6 pir:T11121 T11121

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26854156_f1_2	5138	10360	548	1647	143	7.1e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein H02F09.3	pir:T33369	T33369

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.206.6.9.43...c1...62.....	5139	10361	148	447		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.206.9.6.8.1...f3...45.....	5140	10362	204	615	78	0.014

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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ATP synthase, subunit F	pir:H69227	H69227
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.222.9.6.6.2...f1...6.....	5141	10363	177	534	108	5.4e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:YPI6_CLOPE	P18017
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Description

HYPOTHETICAL 19.7 KD PROTEIN (ORF6)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4409433_c3_95	5142	10364	151	456	85	0.049

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
ORF MSV223 hypothetical protein	gp:AF063866	AF063866

Description

Melanoplus sanguinipes entomopoxvirus, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
831463_c1_56	5143	10365	217	654		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
236.12512_c2_5.....	5144	10366	204	615	141	9.2e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
integrase IntN1	gp:BUU51917	U51917

Description

Bacteroides uniformis insertion element NBUI fragment, integraseIntN1 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24219066_f3_2.....	5145	10367	71	216	52	0.015

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:G3P_SCHMA	P20287

Description

LARVAL SURFACE ANTIGEN) (P-37)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4103388_c3_9	5146	10368	79	240	62	0.0027
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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neuroendocrine protein 7B2	pir:S03938	S03938
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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496.0.925_c3_10	5147	10369	150	450		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5.25.5.16.0_c1_4	5148	10370	72	219		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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5.26.6.8.8.0_c2_7	5149	10371	205	615	276	1.1e-23
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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methyl transferase	gp:STRMTR	L29323
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Description

Streptococcus pneumoniae methyl transferase gene cluster, complete sequence.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2812785_c2_6	5150	10372	276	828	286	3.8e-24

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:BGAL_HUMAN	P16278

Description

GALACTOSIDASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5867213_c1_4	5151	10373	217	654		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1.3.0.8.5.16.2_f2_14.....	5152	10374	362	1089		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2.0.0.8.2.9.6.2_f2_13.....	5153	10375	205	618	384	1.3e-34

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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beta-glucosidase	gp:RAU92808	U92808
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Description

Ruminococcus albus beta-glucosidase (gluA) mRNA, complete cds.
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24644575_c1_33	5154	10376	292	879	227	2.6e-18

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YIBP_ECOLI	P37690

Description

HYPOTHETICAL 46.6 KD PROTEIN IN SECB-TDH INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4476427_c1_34	5155	10377	1050	3153	334	3.3e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
bZIP histidine kinase	gp:PPUY18245	Y18245

Description

Pseudomonas putida todX, todF, todC1, todC2, todB, todA, todD, todE, todG, todI, todH, todS, todT genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5275033_c2_40.....	5156	10378	301	906	232	2.3e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
response regulator DrrA	pir:D72228	D72228

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7129666_f1_1.....	5157	10379	649	1950	914	1.2e-91

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:BGLS_AGRTU	P27034

Description

GLUCOSIDE GLUCOHYDROLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10251900_c1_94	5158	10380	216	651		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1066.2.758..f1..22.....	5159	10381	183	552	271	1.7e-23

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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gp:ATAC006202	AC006202
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Description

Arabidopsis thaliana chromosome II BAC T3B23 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10962692..c2..116.....	5160	10382	194	585	96	0.0022

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein c04040	pir:S75406	S75406
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12194150..f2..41.....	5161	10383	235	708	131	3.9e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:YS29_MYCTU	P71786
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Description

HYPOTHETICAL 27.1 KD PROTEIN CY277.29C
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12687826_f1_16	5162	10384	413	1242	1308	2.2e-133
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
				sp:UXUA_HAEIN	P44488	

Description

MANNONATE DEHYDRATASE, (D-MANNONATE HYDROLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14588387_c3_163	5163	10385	93	282		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1784.05_f1_19.....	5164	10386	131	396		
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20593.76.0_f3_62.....	5165	10387	254	765	228	6.2e-28
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
dihydろdipicolinate reductase				pir:A72246	A72246	

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2189.7192_f1_24.....	5166	10388	324	975	215	3.8e-16
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
hypothetical protein 7				pir:S20799		

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2225275_c2_120	5167	10389	61	186		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22381561_f3_59	5168	10390	411	1236		

Protein name _____ Locus Name _____ Acc# _____

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22851526_f1_6	5169	10391	528	1587	1117	3.8e-113

Protein name _____ Locus Name _____ Acc# _____

hypothetical protein mexF

pir:T30830

T30830

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24005316_f1_15	5170	10392	284	855	696	1.5e-68

Protein name _____ Locus Name _____ Acc# _____

oxidoreductase

gp:NOSHRMA

L37087

Description

Nostoc sp. ATCC 29133 oxidoreductase (hrmU) and HrmA (hrmA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24225682_f1_5	5171	10393	394	1185	493	5.0e-47

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YHIU_ECOLI	P37636

Description

PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24509680_f2_40	5172	10394	312	939	152	7.8e-16

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
prokaryotic type I signal peptidase SipF	gp:AF065159	AF065159

Description

Bradyrhizobium japonicum putative arylsulfatase (arsA), putative soluble lytic transglycosylase precursor (sltA), dihydrodipicolinate synthase (dapA), MscL (mscL), SmpB (smpB), BcpB (bcpB), RnpO (rnpO), RelA/SpoT homolog (relA), PdxJ (pdxJ), and acyl carrier protein synthase AcpS (acpS) genes, complete cds; prokaryotic type I signal peptidase SipF (sipF) gene, sipF-sipS allele,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24615787_f1_7.....	5173	10395	491	1476	503	4.4e-48

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
OprM	gp:AB011381	AB011381

Description

Pseudomonas aeruginosa gene for OprM, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24651437_f3_60.....	5174	10396	312	939	247	5.9e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein	pir:H72417	H72417

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25820437_f3_56	5175	10397	564	1695	827	9.8e-85

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein mexF	pir:T30830	T30830

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26.3.6.0.7.17_c1_109	5176	10398	208	627	321	8.5e-29

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
phosphoglycolate phosphatase (gph) homolog	pir:C70184	C70184

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26.6.17.128_f2_47	5177	10399	171	516	354	2.7e-32

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
polysialic acid capsule expression protein	pir:B70434	B70434

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26.6.7.8.200_f2_27	5178	10400	1030	3093	1827	2.2e-188

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
beta-galactosidase	gp:AF055482	AF055482

Description

Thermotoga neapolitana galactose utilization operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.0.01251_c1_93	5179	10401	450	1353		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33593963_c2_136	5180	10402	74	225		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
33625658_f2_3.0.....	5181	10403	275	828	453	8.7e-43

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:LPXA_ECOLI		
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Description

(EC 2.3.1.129) (UDP-N-ACETYLGLUCOSAMINE ACYLTRANSFERASE)						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34022832_c3_14.7.....	5182	10404	433	1302	508	1.3e-48

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:YMXG_BACSU	Q04805
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Description

HYPOTHETICAL PROCESSING PROTEASE, (ORFP)						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4484712_f1_14.....	5183	10405	498	1497	173	1.5e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:LEP_SALTY	P23697
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Description

SIGNAL PEPTIDASE I, (SPASE I) (LEADER PEPTIDASE I)						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
549091_c3_174	5184	10406	112	339		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6.0356.75..f2..49.....	5185	10407	371	1116	295	4.8e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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protein-tyrosine phosphatase	gp:AB028630	AB028630
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Description

Clostridium perfringens hyp27, bacH, ptp, cpd genes for hypothetical protein, bacterial hemoglobin, protein-tyrosinephosphatase, 2', 3'-cyclic nucleotide 2'-phosphodiesterase,partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6.83.7.782..c1..96.....	5186	10408	214	645		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
8.47.9.0..f3..73.....	5187	10409	485	1455	880	4.9e-88

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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ATP-dependent RNA helicase homolog ydbR	pir:D69772	D69772
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12402186_c3_12	5188	10410	144	432		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15628378_c1_8	5189	10411	375	1128	356	4.5e-32

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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histidine kinase	gp:AF114442	AF114442
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Description

Nostoc punctiforme histidine kinase (hepK) gene, complete cds.						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23633456_c3_10	5190	10412	124	375	302	2.6e-26

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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2,3-bisphosphoglycerate-independent	gp:AF120091	AF120091
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Description

Bacillus stearothermophilus 2,3-bisphosphoglycerate-independentphosphoglycerate mutase (pgm) gene, complete cds.						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10554662_c3_32	5191	10413	186	561	212	3.0e-17

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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sp:YP20_BACLI	P05332
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Description

HYPOTHETICAL P20 PROTEIN						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11777161_c3_65	5192	10414	65	198		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
146.48512_f3_34.....	5193	10415	115	348	280	1.9e-24

Protein name Locus Name Acc#

hypothetical protein MTH1452 pir:D69060 D69060

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
166.76505_c2_62.....	5194	10416	404	1215	226	2.7e-16

Protein name Locus Name Acc#

probable hydrolase pir:T37132 T37132

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
168.32885_f3_43.....	5195	10417	310	933	1023	3.5e-103

Protein name Locus Name Acc#

hypothetical protein pir:JQ1020 JQ1020

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
196.10637_f1_6.....	5196	10418	229	690		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19728433_c1_49	5197	10419	429	1290	244	4.2e-18

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
DNA damage-inducible protein. PAB1438	pir:C75053	C75053

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2286.0128..f1_8.....	5198	10420	83	252	64	0.031

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:SPRC_XENLA	P36378

Description

(OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40)						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
236.01.000..f1_3.....	5199	10421	84	255	75	0.039

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
FAA	gp:AC005565	AC005565

Description

Homo sapiens chromosome 16, cosmid clone 444B9 (LANL), complete sequence.						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2441.06.87..c2_63.....	5200	10422	231	696		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24415902_f2_18	5201	10423	630	1893		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
246.25.3.11_f3_42.....	5202	10424	277	834	1272	1.4e-129

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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7-alpha-hydroxysteroid dehydrogenase	gp:AF173833	AF173833
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Description

Bacteroides fragilis 7-alpha-hydroxysteroid dehydrogenase (hhdA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24.726.53.7_f3_39.....	5203	10425	71	216	56	0.021

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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hypothetical protein C0510w	pir:T18460	T18460
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
256.00.25.0_c2_57.....	5204	10426	320	963		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26305349_c1_44	5205	10427	90	273	156	3.5e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:FE0B_METJA	Q57986

Description

FERROUS IRON TRANSPORT PROTEIN B HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26595317_c2_59	5206	10428	156	471	302	8.7e-27

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein SCI30A.19	pir:T36799	T36799

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3.6150277..f1.5.....	5207	10429	286	861	199	6.9e-15

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
transcription regulator AraC/XylS family homolog ydeE	pir:G69777	G69777

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4.9533.87..c2..5.8.....	5208	10430	134	405	279	2.4e-24

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YUXK_BACSU	

Description

HYPOTHETICAL 15.7 KD PROTEIN IN PBPD-COMA INTERGENIC REGION (ORF2)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6048462_f3_35	5209	10431	245	738	573	1.7e-55

Protein name	Locus Name	Acc#
	sp:UNG_HUMAN	P13051

Description

URACIL-DNA GLYCOSYLASE PRECURSOR, (UDG)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6053437_c3_71	5210	10432	1062	3189	564	2.2e-87

Protein name	Locus Name	Acc#
115K outer membrane protein precursor:SusC protein	pir:JC6027	JC6027

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6.7.3.5.8.4.1_f2_25.....	5211	10433	105	318	444	7.8e-42

Protein name	Locus Name	Acc#
hypothetical protein	pir:JQ1020	JQ1020

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6.8.3.7.8.3.7_c2_6.0.....	5212	10434	246	741	285	5.5e-25

Protein name	Locus Name	Acc#
	sp:YTFE_HAEIN	P45312

Description

HYPOTHETICAL PROTEIN HI1677

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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24417250_f3_7	5213	10435	67	204	79	0.029
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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OmpK37 porin	gp:KPN011502	AJ011502
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Description

Klebsiella pneumoniae (strain SD8) ompK37 gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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6725192_f3_6	5214	10436	815	2448	159	3.1e-12
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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colicin I receptor	gp:ECOCIR
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Description

E.coli colicin I receptor gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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20.06.400_f2_5.....	5215	10437	74	225		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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3218942_f1_1.....	5216	10438	134	405		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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34408328_f2_4	5217	10439	399	1200		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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4179.002_f3_9.....	5218	10440	144	435		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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15625252_f1_1.....	5219	10441	253	762		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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2772937_f1_2.....	5220	10442	360	1083	526	1.4e-51
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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115K outer membrane protein precursor: SusC protein	pir:JC6027	JC6027
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Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
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35351583_c1_3.....	5221	10443	71	216		
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<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
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Description

NO-HIT						
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<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36038302_c3_12	5222	10444	752	2256	148	5.9e-07
<u>Protein name</u>				<u>Locus Name</u>	<u>Acc#</u>	
conserved hypothetical protein yknZ				pir:E69858	E69858	
<u>Description</u>	<hr/>					